



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 138972

**TO: Patricia Duffy**  
**Art Unit: 1645**  
**Location: rem/3B05/3C18**  
**Serial Number: 10063551**

**Wednesday, July 20, 2005**

**From: Beverly Shears**  
**Location: Biotech-Chem Library**  
**REM 1A54**  
**Phone: 571-272-2528**  
**beverly.shears@uspto.gov**

### Search Notes

#### Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**This Page Blank (uspto)**

STIC-Biotech/ChemLib

CRFE

158972

119

From: Duffy, Patricia  
Sent: Tuesday, July 12, 2005 10:08 AM  
To: STIC-Biotech/ChemLib  
Subject: SPDI search

IN re: 10/063,551

Please search SEQ ID NO:46.  
Standard SPDI output.

Patricia A. Duffy, Ph.D.  
Art Unit 1645  
Remsen 3B05; Mailbox 3C18  
571-272-0855

\*\*\*\*\*  
STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

Date completed: \_\_\_\_\_

Searcher: Beverly e 2528

Terminal time: \_\_\_\_\_

Elapsed time: \_\_\_\_\_

CPU time: \_\_\_\_\_

Total time: \_\_\_\_\_

Number of Searches: \_\_\_\_\_

Number of Databases: \_\_\_\_\_

Search Site

\_\_\_\_\_ STIC

\_\_\_\_\_ CM-1

\_\_\_\_\_ Pre-S

Type of Search

\_\_\_\_\_ N.A. Sequence

\_\_\_\_\_ A.A. Sequence

\_\_\_\_\_ Structure

\_\_\_\_\_ Bibliographic

Vendors

\_\_\_\_\_ IG

\_\_\_\_\_ STN

\_\_\_\_\_ Dialog

\_\_\_\_\_ APS

\_\_\_\_\_ Geninfo

\_\_\_\_\_ SDC

\_\_\_\_\_ DARC/Questel

✓ Other CGN

**This Page Blank (uspto)**



GenCore version 5.1.6

OM protein - protein search, using sw model  
Run on: July 14, 2005, 13:23:54 ; Search time 164 Seconds  
(without alignments)  
790.029 Million cell updates/sec

Title: US-10-063-551-46  
Perfect score: 1772  
Sequence: 1 MAGSPTCLTILVILWQLTGS.....PHSLLTMDTPRLPAYENVI 335  
Scoring table: BLOSUM62  
Searched: Gapop 10.0 , Gapext 0.5  
Total number of hits satisfying chosen parameters: 2105692  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : A Geneseq 16Dec04:

- 1: geneseqp1980s:
- 2: geneseqp1990s:
- 3: geneseqp2000s:
- 4: geneseqp2001s:
- 5: geneseqp2002s:
- 6: geneseqp2003as:
- 7: geneseqp2003bs:
- 8: geneseqp2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description

RESULT 1  
ID AAY66701 standard; protein; 335 AA.

DE Membrane-bound protein PRO1138.

PN WO9963088-A2.

PD 09-DEC-1999.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 3; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 2

ID AAY70431 standard; protein; 335 AA.

DE Human cell surface immunomodulator-1 (CSIMM-1).

PN WO200011150-A1.

PD 02-MAR-2000.

PA (INCY-) INCYTE PHARM INC.

Query Match 100.0%; Score 1772; DB 3; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 3

ID AAY44609 standard; protein; 335 AA.

DE Human myocardium protein-7.

PN WO9967387-A2.

PD 29-DEC-1999.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match 100.0%; Score 1772; DB 3; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 4

ID AAU29119 standard; protein; 335 AA.

DE Human PRO polypeptide sequence #96.

PN WO200168848-A2.

PD 20-SEP-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 5

ID AAB87548 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 4; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 6

ID AAB47321 standard; protein; 335 AA.

DE Human PRO1138.

DE Novel human secreted or transmembrane protein PRO1138.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 17  
ID ABU82629 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 18  
ID ABU82801 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 19  
ID ABU89922 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 20  
ID ABR68171 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 21  
ID ABU60548 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein, #100.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 22  
ID ABU96224 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 23  
ID ABU92655 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 24  
ID AB008732 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 25  
ID AB002784 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 26  
ID ABR74938 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 27  
ID ABR94700 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 28  
ID ABU13930 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 29  
ID ABU85673 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 30  
ID ABU98933 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 31  
ID ABU98048 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 32  
ID ABU91754 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 33  
ID ABU89447 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 34  
ID ABU86288 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 35  
ID ABU67501 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 36  
ID ABU80529 standard; protein; 335 AA.

DE Human PRO protein #96.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 37  
ID ABU72515 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003035331-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 38  
ID ABU90898 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 39  
ID ABO33957 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO138.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 40  
ID ABR99447 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 41  
ID ABR98837 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 42  
ID ABO16360 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 43  
ID ABR92260 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 44  
ID ABO18901 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 45  
ID ABR78322 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 46  
ID ABU71974 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO138.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 47  
ID ABU85058 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 48  
ID ABO00197 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 49  
ID ABO11529 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 50  
ID ABO02174 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 51  
ID ABU88748 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 52  
ID ABU83443 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 53  
ID ABO06244 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 54  
ID ABR59280 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 55  
ID ABO09342 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 56  
ID ABO19206 standard; protein; 335 AA.

DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 57  
ID ABO1124 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 58  
ID ABR66842 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 59  
ID ABR66842 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 60  
ID ABO13761 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US200304916-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 61  
ID ABU71528 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 62  
ID ABU65664 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein, SEQ ID 192.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 63  
ID ABO07512 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 64  
ID ABO03699 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 65  
ID ABR67147 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 66  
ID ABO15750 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.

PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 67  
ID ABU56031 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein, PRO1138.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 68  
ID ABU72309 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 69  
ID ABU65359 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 70  
ID ABU95304 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 71  
ID ABU71207 standard; protein; 335 AA.  
DE Human PRO1138 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 72  
ID ABO07817 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 73  
ID ABR70058 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 74  
ID ABR69391 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 75  
ID ABO01532 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 76  
ID ABU81334 standard; protein; 335 AA.

DE Human PRO polypeptide #96.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 77  
ID ABR60131 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 78  
ID ABUS0982 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 79  
ID ABR67866 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 80  
ID ABR65254 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 81  
ID ABR68476 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 82  
ID ABR71888 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 83  
ID ABUS59264 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein, #100.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 84  
ID ABUS5368 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 85  
ID ABUS9058 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 86  
ID ABUS3138 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.

PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 87  
ID ABUS4994 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 88  
ID ABUS0542 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 89  
ID ABUS4053 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 90  
ID ABUS3704 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 91  
ID ABO25961 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 92  
ID ABR64949 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 93  
ID ABO27303 standard; protein; 335 AA.  
DE Human secreted/transmembrane polypeptide PRO138.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 94  
ID ABR68781 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 95  
ID ABO06597 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 96  
ID ABR99142 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 97  
ID ABUS7026 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 98  
ID ABUS85978 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 99  
ID ABUS2265 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 100  
ID ABUS7276 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 101  
ID ABUS3748 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 102  
ID ABUS8122 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 103  
ID ABUS2498 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 104  
ID ABUS1833 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 105  
ID ABUS65997 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 106  
ID ABUS1168 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138.  
PN US2003027212-A1.  
PD 06-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 107  
ID ABR59826 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 108  
ID ABUS4014 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 109  
ID ABUS9867 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 110  
ID ABR6537 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 111  
ID ABR90955 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 112  
ID ABO53283 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO138.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 113  
ID ABUS8970 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein, #100.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 114  
ID ABUS4382 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 115  
ID ABUS79264 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 116  
ID ABUS6593 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032129-A1.

PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 117  
ID AB08698 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 118  
ID AB094687 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 119  
ID ABO04614 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 120  
ID ABR70363 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 121  
ID AB092348 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032187-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 122  
ID AB098528 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032301-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 123  
ID ABR65927 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 124  
ID ABR64644 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 125  
ID AB059413 standard; protein; 335 AA.  
DE Novel human secreted or transmembrane protein PRO1054.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 126  
ID AB079569 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 127  
ID AB092960 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 128  
ID AB095919 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 129  
ID AB091139 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 130  
ID AB090232 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 131  
ID ABO09647 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 132  
ID ABR58417 standard; protein; 335 AA.  
DE Human NOV27a.  
PN WO2003029423-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 133  
ID ABO10919 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 134  
ID ABR70973 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 135  
ID AB098285 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 136  
ID AB087581 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;

RESULT 137  
ID ABU91449 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 138  
ID ABU89290 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 139  
ID ABU84663 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 140  
ID ABR69753 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 141  
ID ABU80130 standard; protein; 335 AA.  
DE Human PRO protein #96.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 142  
ID ABU82497 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 143  
ID ABU92179 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 144  
ID ABU93399 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 145  
ID ABO09952 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 146  
ID ABO09037 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 147  
ID ABO08427 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044922-A1.

ID ABU96461 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 148  
ID ASU10885 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 149  
ID ABU10605 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein #96.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 150  
ID ABU81637 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 151  
ID ABU72131 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 152  
ID ABU95614 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 153  
ID ABU96823 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 154  
ID ABR70668 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 155  
ID ABO05019 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 156  
ID ABO08427 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044922-A1.



PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 157  
ID ABU88576 standard; protein; 335 AA.  
DE Human secreted and transmembrane polypeptide PRO1138.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 158  
ID ABO34090 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 159  
ID ABO05634 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 160  
ID ABR74023 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 161  
ID ABR95615 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 162  
ID ABR80912 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 163  
ID ABR81217 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 164  
ID ABR00913 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 165  
ID ABR88515 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 166  
ID ABO03089 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.

ID ABW7336 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 167  
ID ABO28820 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 168  
ID ABO31565 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 169  
ID ABO07982 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 170  
ID ABO40462 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 171  
ID ABO35887 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 172  
ID ABO4026 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 173  
ID ADA7944 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 174  
ID ABO24821 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 175  
ID ABO03089 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.



ID ABM11642 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 195  
ID ABM02743 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 196  
ID ABM16039 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 197  
ID ABO27600 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 198  
ID ABM29091 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 199  
ID ABM07067 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 200  
ID ABM21161 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 201  
ID ABM09507 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 202  
ID ABO41377 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 203  
ID ABO36192 standard; protein; 335 AA.

DE Human PRO polypeptide #96.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 204  
ID ABO43721 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 205  
ID ABM76421 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 206  
ID ABM76117 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 207  
ID ABM25736 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 208  
ID ABM26041 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 209  
ID ADA21450 standard; protein; 335 AA.  
DE Human secreted/transmembrane polypeptide PRO1138.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 210  
ID ABO03394 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 211  
ID ABO02479 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 212  
ID ABO44261 standard; protein; 335 AA.  
DE Human secreted/transmembrane polypeptide PRO 1138.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 213

ID ABR90650 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 214  
ID ABR73718 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 215  
ID ABO16970 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
FN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 216  
ID ABR94395 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 217  
ID ABR75902 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 218  
ID ABR71278 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 219  
ID ABR93175 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 220  
ID ABR93480 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 221  
ID ADA10237 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein, PRO1138.  
FN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 222  
ID ABR87905 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 223  
ID ABO27905 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
FN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 224  
ID ABO30040 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
FN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 225  
ID ABO33249 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
FN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 226  
ID ABO4937 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 227  
ID ABO8897 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 228  
ID ABO36497 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
FN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 229  
ID ABO35582 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
FN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 230  
ID ABO39547 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
FN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 231  
ID ABO10422 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 232  
ID ABM11947 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 233  
ID ABO52093 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 234  
ID ABO52398 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 235  
ID ADAL1908 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 236  
ID ABO23716 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 237  
ID ADB17291 standard; protein; 335 AA.  
DE Human transmembrane PRO polypeptide (SeqID 46).  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 238  
ID ADAL1781 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 239  
ID ABR97202 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 240  
ID ABR86990 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 241  
ID ABM11032 standard; protein; 335 AA.

DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 242  
ID ABM28176 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 243  
ID ABO32175 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 244  
ID ABM15302 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 245  
ID ABM06457 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 246  
ID ABM04268 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 247  
ID ABM22381 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 248  
ID ABM07677 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 249  
ID ABO40767 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 250  
ID ABM35414 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 251  
ID ABW33177 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 252  
ID AB052703 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 253  
ID AB050263 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 254  
ID ABU99257 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 255  
ID AB004309 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003031614-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 256  
ID AB005939 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 257  
ID ABM18479 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 258  
ID ADA27889 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 259  
ID ABR97507 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 260  
ID ABR0607 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 261  
ID ABM01218 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 262  
ID ABR88820 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 263  
ID ABM13472 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 264  
ID ABM20856 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 265  
ID ABO41987 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 266  
ID ABO42597 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 267  
ID ABM10117 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 268  
ID ABO38632 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 269  
ID ABM32872 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 270  
ID BM22686 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 271  
ID BM74897 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 272  
ID ADA79736 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 273  
ID ABR96287 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 274  
ID BM02438 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 275  
ID ABR86380 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 276  
ID ABR86685 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 277  
ID BM16649 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 278  
ID BM29701 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 279  
ID ABO29125 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 280  
ID BM23906 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 281  
ID BM23296 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 282  
ID BM22076 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 283  
ID ABO37717 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 284  
ID BM28481 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 285  
ID BM28786 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 286  
ID ARM66430 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 287  
ID BM75812 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 288  
ID BM34092 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.





DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 06-FEB-2003.  
ID ABO16665 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 06-FEB-2003.  
ID ABO18291 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 06-FEB-2003.  
ID ABO22718 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 06-FEB-2003.  
ID ABO23023 standard; protein; 335 AA.  
DE Human secreted polypeptide #96.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 03-APR-2003.  
ID ABR92565 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 03-APR-2003.  
ID ABR81522 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 13-MAR-2003.  
ID ABM77946 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 13-MAR-2003.  
ID ABR99735 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 17-APR-2003.  
ID ABM26651 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 13-FEB-2003.

RESULT 317  
ID ABM13777 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 03-APR-2003.  
ID ABO28515 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 03-APR-2003.  
ID ABO30345 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 03-APR-2003.  
ID ABO7372 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 10-APR-2003.  
ID ABO3963 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 10-APR-2003.  
ID ABO37107 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 10-APR-2003.  
ID ABO41682 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 10-APR-2003.  
ID ABO35277 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 10-APR-2003.  
ID ABM25126 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
PD 05-JUN-2003.  
ID ABO47518 standard; protein; 335 AA.

DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 327  
ID ABO47823 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 328  
ID ABO48433 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 329  
ID ABO51483 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 330  
ID ABO51788 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 331  
ID ABO50568 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 332  
ID ABR79692 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 333  
ID ABM16954 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 334  
ID ABO17986 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 335  
ID ABO20938 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032132-A1.  
PD 13-FEB-2003.

Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 336  
ID ABR96897 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 337  
ID ADA38694 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 338  
ID ABM12252 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 339  
ID ABM16344 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 340  
ID ABM24211 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 341  
ID ABM14692 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 342  
ID ABM04573 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 343  
ID ABM06762 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 344  
ID ABM09202 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 345  
ID ABO39242 standard; protein; 335 AA.

DE Human secreted/transmembrane protein (PRO) #96.  
FN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 346  
ID ABM75507 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 347  
ID ABM25431 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003104541-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 348  
ID ABM19941 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 349  
ID ABO46847 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
FN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 350  
ID ABO47152 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
FN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 351  
ID ADA83261 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
FN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 352  
ID ABR71583 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 353  
ID ABR72193 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 354  
ID ABR98532 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 355  
ID ABO69902 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
FN US2003040053-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 356  
ID ABR84855 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003040057-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 357  
ID ABR73413 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 358  
ID ABR76507 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003044932-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 359  
ID ABR73108 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003027270-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 360  
ID ABM18174 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 361  
ID ABO20633 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
FN US2003032126-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 362  
ID ABO25376 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
FN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 363  
ID ABO25681 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
FN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 364  
ID ABR94090 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003059879-A1.  
PD 27-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 365  
ID ADA92815 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 366  
ID ABR79997 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 367  
ID ABM11337 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 368  
ID ABO32944 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 369  
ID ABO30650 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 370  
ID ABO30955 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 371  
ID ABM27261 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 372  
ID ABM30006 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 373  
ID ABM05542 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 374  
ID ABM15607 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 375  
ID ABM0592 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 376  
ID ABO42292 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 377  
ID ABO38022 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 378  
ID ABO45932 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 379  
ID ABM66735 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 380  
ID ADB20304 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 381  
ID ABM19636 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 382  
ID ABO49348 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 383  
ID ABO49653 standard; protein; 335 AA.

DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 384  
ID ADA78556 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 385  
ID ABR88210 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 386  
ID ADA00377 standard; protein; 335 AA.  
DE Human secreted/transmembrane polypeptide PRO 138.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 387  
ID ABR26956 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 388  
ID ABR03353 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 389  
ID ABO39852 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;  
RESULT 390  
ID ABO49958 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 391  
ID ABO50873 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 392  
ID ABO05329 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.

PN US2003036126-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 393  
ID ABR74633 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 394  
ID ABR77112 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 395  
ID ABR17869 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 396  
ID ABR95920 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 397  
ID ABO21853 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 398  
ID ABO20023 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 399  
ID ABO24326 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 400  
ID ABR86075 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 401  
ID ABR10727 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 402  
ID ABR76726 standard; protein; 335 AA.

DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 403  
ID ABR89430 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 404  
ID ABM12557 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 405  
ID ABM05847 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 406  
ID AB034972 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 407  
ID ABM03048 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 408  
ID ABM19026 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 409  
ID ABM19331 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 410  
ID ABO46542 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 411  
ID AB049043 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049757-A1.

PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 412  
ID ABR69086 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 413  
ID ABR89125 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 414  
ID ABR72498 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 415  
ID ABR74328 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 416  
ID ABO18596 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 417  
ID ABR80302 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 418  
ID ABM01523 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 419  
ID ABM02133 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 420  
ID ABR87295 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 421  
ID ABO49043 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049757-A1.

ID ABM12862 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 422  
ID ABM30616 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 423  
ID ABM24516 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 424  
ID ABO29430 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 425  
ID ABO31260 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 426  
ID ABM14387 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 427  
ID ABM09812 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 428  
ID ABO38937 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 429  
ID ABM34702 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 430  
ID ABO51178 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.

PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 431  
ID ABO04004 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 432  
ID ABO10474 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 433  
ID ABO53176 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 434  
ID ABR77717 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 435  
ID ABR78927 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 436  
ID ABO24021 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 437  
ID ABR93785 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 438  
ID ABM01828 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 439  
ID ABM78251 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 440  
ID ABO51178 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.

ID ABR90040 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 441  
ID AD22376 standard; protein; 335 AA.  
DE Human secreted/transmembrane polypeptide PRO1138.  
FN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 442  
ID ABM27566 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 443  
ID ABM13167 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 444  
ID ABO31870 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
FN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 445  
ID ABM14082 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 446  
ID ABM08287 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 447  
ID ABO40157 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
FN US2003068681-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 448  
ID ABM74592 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 449  
ID ABM33787 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003096358-A1.  
PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 450  
ID ABM20246 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 451  
ID ABO48738 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
FN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 452  
ID ABO22546 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
FN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 453  
ID ABR72803 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 454  
ID ABO15445 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
FN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 455  
ID ABR85160 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 456  
ID ABO15140 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
FN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 457  
ID ABO17275 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
FN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 458  
ID ABM17564 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
FN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 459  
ID ADA06542 standard; protein; 335 AA.  
DE Human secreted/transmembrane PRO polypeptide #71.  
FN US2003049638-A1.



PD 13-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 460  
ID ADA39235 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 461  
ID ABR85465 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 462  
ID ABW77031 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 463  
ID ABO28210 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 464  
ID ABM22991 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 465  
ID ABM30311 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 466  
ID ABM21771 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 467  
ID ABM21466 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 468  
ID ABM14997 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 469  
ID ABO41072 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 470  
ID ABO36802 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 471  
ID ABO37412 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 472  
ID ABM75202 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 473  
ID ABM33482 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 474  
ID ABO46237 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 475  
ID ADA82627 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 476  
ID AD885619 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 477  
ID ADB96261 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 478

ID ABM31836 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068680-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 479  
ID ABM311226 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 480  
ID ADB85935 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 481  
ID ABM32141 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 482  
ID ABM32446 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 483  
ID ADB68298 standard; protein; 335 AA.  
DE Human PRO1138 protein.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 484  
ID ADB68105 standard; protein; 335 AA.  
DE Human PRO1138 protein.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 485  
ID ABM31531 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 486  
ID ABM30921 standard; protein; 335 AA.  
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 487  
ID ADB90922 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.

PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 488  
ID ADC57733 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 489  
ID ADC55097 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 490  
ID ADC11964 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 491  
ID ADC07002 standard; protein; 335 AA.  
DE Human PRO1138 protein.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 492  
ID ADC56386 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 493  
ID ADC17181 standard; protein; 335 AA.  
DE Mammalian PRO polypeptide (SeqID 46).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 494  
ID ADC07441 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 495  
ID ADC11431 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 496  
ID ADC14879 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 497  
ID ADC52374 standard; protein; 335 AA.

DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003138982-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 498  
ID ADC14553 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 499  
ID ADD08085 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 500  
ID ADC81910 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 501  
ID ADD07552 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 502  
ID ADC82443 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 503  
ID ADD05665 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 504  
ID ADD08623 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 505  
ID ADD06872 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 506  
ID ADC89503 standard; protein; 335 AA.  
DE Human natural killer cell surface receptor CS1.  
PN US2003113332-A1.  
PD 19-JUN-2003.  
PA (UNYT-) UNIV NORTH TEXAS HEALTH SCI CENT.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;

RESULT 507  
ID ADC83119 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 508  
ID ADD67525 standard; protein; 335 AA.  
DE Human Ly1728P protein SEQ ID NO:2.  
PN WO2003062401-A2.  
PD 31-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 509  
ID ADD55226 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 510  
ID ADD36050 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 511  
ID ADD56184 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 512  
ID ADD54622 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 513  
ID ADE26776 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 514  
ID ADE26243 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 515  
ID ADF67180 standard; protein; 335 AA.  
DE Human PRO1138 amino acid sequence SEQ ID NO:253.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
Pred. No. 9.2e-163;  
RESULT 516  
ID ADG01051 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 517  
ID ADG08604 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
FN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 518  
ID ADG02660 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
FN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 519  
ID ADG01367 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
FN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 520  
ID ADF95542 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
FN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 521  
ID ADF95225 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
FN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 522  
ID ADG12357 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
FN US2003207392-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 523  
ID ADH24078 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
FN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 524  
ID ADH34104 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
FN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 525  
ID ADH29937 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
FN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 526  
ID ADH23908 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
FN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 527  
ID ADH09017 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
FN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 528  
ID ADG85312 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
FN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 529  
ID ADH24588 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
FN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 530  
ID ADH37444 standard; protein; 335 AA.  
DE Human secreted and transmembrane protein PRO138 cDNA.  
FN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 531  
ID ADH02033 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
FN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 532  
ID ADH37614 standard; protein; 335 AA.  
DE Human secreted and transmembrane protein PRO138 cDNA.  
FN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 533  
ID ADG85652 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
FN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 534  
ID ADH24248 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
FN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 535  
ID ADH24248 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
FN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

ID ADH38542 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 536  
ID ADG83663 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 537  
ID ADH29471 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 538  
ID ADH27587 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 539  
ID ADH37784 standard; protein; 335 AA.  
DE Human secreted and transmembrane protein PRO1138 cDNA.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 540  
ID ADH37961 standard; protein; 335 AA.  
DE Human secreted and transmembrane protein PRO1138 cDNA.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 541  
ID ADH57381 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 542  
ID ADH53523 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 543  
ID ADH53693 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 544  
ID ADH52029 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181697-A1.

DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 545  
ID ADH49884 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 546  
ID ADI25394 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 547  
ID ADH90187 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 548  
ID ADI25564 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 549  
ID ADH97738 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 550  
ID ADI35434 standard; protein; 335 AA.  
DE Human PRO polypeptide #71.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 551  
ID ADI03586 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 552  
ID ADI11943 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 553  
ID ADH90017 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181697-A1.

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 554  
ID ADH99926 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 555  
ID ADH98418 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 556  
ID ADI11093 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 557  
ID ADI11603 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 558  
ID ADH98248 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 559  
ID ADH98588 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 560  
ID ADH98078 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 561  
ID ADI05066 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 562  
ID ADI03416 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 563  
ID ADI04811 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 564  
ID ADH78265 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181668-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 565  
ID ADI19609 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 566  
ID ADH90357 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 567  
ID ADI03076 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 568  
ID ADH77925 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 569  
ID ADH97908 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 570  
ID ADI01293 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 571  
ID ADI01988 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;  
RESULT 572  
ID ADI03416 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 572  
ID ADI03246 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 573  
ID ADI11433 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 574  
ID ADI02335 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 575  
ID ADI11773 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 576  
ID ADI05410 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 577  
ID ADH79482 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 578  
ID ADI19439 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 579  
ID ADI05240 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 580  
ID ADH79652 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 581  
ID ADI01478 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 582  
ID ADI01648 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 583  
ID ADI01818 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 584  
ID ADH79822 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 585  
ID ADI04640 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 586  
ID ADI02776 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 587  
ID ADH78095 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 588  
ID ADI25734 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 589  
ID ADI25904 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 590  
ID ADI25904 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

ID ADK5416 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 591  
ID ADH98758 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 592  
ID ADH79999 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 593  
ID ADJ32798 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 594  
ID ADM30332 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 595  
ID ADJ93730 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 7; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 596  
ID ADC52184 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 597  
ID ADH74329 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 598  
ID ADE74941 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein (PRO) #96.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 599  
ID ADF35379 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2003194760-A1.

PD 16-OCT-2003.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 600  
ID ADG11629 standard; protein; 335 AA.  
DE Human PRO1138 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 601  
ID ADF96154 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 602  
ID ADG04425 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 603  
ID ADG00585 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 604  
ID ADH06616 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 605  
ID ADH06446 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 606  
ID ADG68867 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 607  
ID ADH27757 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 608  
ID ADH25098 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;



Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 609  
ID ADH33730 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 610  
ID ADG82841 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 611  
ID ADH02373 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 612  
ID ADH07980 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 613  
ID ADG69377 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 614  
ID ADH39198 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 615  
ID ADH26122 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 616  
ID ADG83938 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 617  
ID ADH1499 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 618  
ID ADG85482 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 619  
ID ADH06276 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 620  
ID ADH30106 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 621  
ID ADH24418 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 622  
ID ADH33091 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 623  
ID ADG69547 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 624  
ID ADH07810 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 625  
ID ADG85822 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 626  
ID ADH39368 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

ID ADH33560 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 628  
ID ADH33900 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 629  
ID ADH01110 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 630  
ID ADG69717 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 631  
ID ADH20992 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US200324358-A1.  
PD 04-DEC-2003.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 632  
ID ADH02203 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 633  
ID ADG69207 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 634  
ID ADG85992 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 635  
ID ADH24928 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 636  
ID ADH39545 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.

PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 637  
ID ADH20032 standard; protein; 335 AA.  
DE Human secreted/transmembrane protein PRO1138.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 638  
ID ADH02543 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 639  
ID ADG69037 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 640  
ID ADH07640 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 641  
ID ADG86162 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 642  
ID ADH24758 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 643  
ID ADH25806 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 644  
ID ADH38372 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 645  
ID ADH57211 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181642-A1.

PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 646  
ID ADH52199 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 647  
ID ADH49565 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 648  
ID ADH90527 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 649  
ID ADI11263 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 650  
ID ADH98928 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 651  
ID ADI02158 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003190699-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 652  
ID ADH90697 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 653  
ID ADJ54830 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 654  
ID ADJ98572 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003187197-A1.  
PD 02-OCT-2003.

PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 655  
ID ADJ98742 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 656  
ID ADH78901 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 657  
ID ADJ99135 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 658  
ID ADJ99305 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 659  
ID ADJ98923 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 660  
ID ADH79071 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 661  
ID ADK00931 standard; protein; 335 AA.  
DE Human PRO polypeptide #23.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 662  
ID ADK14452 standard; protein; 335 AA.  
DE Novel human secreted and transmembrane protein PRO1138.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1772; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
RESULT 663  
ID ADJ64601 standard; protein; 335 AA.  
DE Human PRO polypeptide #96.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 8; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
 RESULT 664  
 ID ADM311497 standard; protein; 335 AA.  
 DE Novel human secreted and transmembrane protein PRO1138.  
 PN US2004048334-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1772; DB 8; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
 RESULT 665  
 ID ADM36544 standard; protein; 335 AA.  
 DE Novel human secreted and transmembrane protein PRO1138.  
 PN US2004053358-A1.  
 PD 18-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1772; DB 8; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
 RESULT 666  
 ID ADM40349 standard; protein; 335 AA.  
 DE Novel human secreted and transmembrane protein PRO1138.  
 PN US2004048335-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1772; DB 8; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
 RESULT 667  
 ID ADM80901 standard; protein; 335 AA.  
 DE Human PRO polypeptide #23.  
 PN US2004058411-A1.  
 PD 25-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1772; DB 8; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
 RESULT 668  
 ID ADM37957 standard; protein; 335 AA.  
 DE Novel human secreted and transmembrane protein PRO1138.  
 PN US2004091959-A1.  
 PD 13-MAY-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1772; DB 8; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
 RESULT 669  
 ID AAB32373 standard; protein; 336 AA.  
 DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:59.  
 PN WO2000047602-A1.  
 PD 17-AUG-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 100.0%; Score 1772; DB 3; Length 336;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-163;  
 RESULT 670  
 ID ADP18672 standard; protein; 335 AA.  
 DE Human disease related protein SeqID103.  
 PN WO2003018621-A2.  
 PD 06-MAR-2003.  
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
 Query Match 99.8%; Score 1769; DB 7; Length 335;  
 Best Local Similarity 99.7%; Pred. No. 1.8e-162;  
 RESULT 671  
 ID ADU69599 standard; protein; 335 AA.  
 DE Human heat mitochondrial protein as a therapeutic target SeqID1405.  
 PN WO2003087768-A2.  
 PD 23-OCT-2003.  
 PA (MITO-) MITOKOR.  
 PA (BUCK-) BUCK INST AGE RES.  
 Query Match 99.8%; Score 1769; DB 7; Length 335;  
 Best Local Similarity 99.7%; Pred. No. 1.8e-162;  
 RESULT 672  
 ID ABR58418 standard; protein; 348 AA.  
 DE Human NOV27b.  
 PN WO2003029423-A2.  
 PD 10-APR-2003.  
 PA (CURA-) CURAGEN CORP.

Query Match 99.1%; Score 1755.5; DB 6; Length 348;  
 Best Local Similarity 96.3%; Pred. No. 3.9e-161;  
 RESULT 673  
 ID AAY44610 standard; protein; 312 AA.  
 DE Mature human myocardium protein-7.  
 PN WO9967387-A2.  
 PD 29-DEC-1999.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 93.3%; Score 1653; DB 3; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-151;  
 RESULT 674  
 ID ABB97473 standard; protein; 328 AA.  
 DE Novel human protein SEQ ID NO: 741.  
 PN WO200222660-A2.  
 PD 21-MAR-2002.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 78.6%; Score 1392.5; DB 5; Length 328;  
 Best Local Similarity 86.4%; Pred. No. 5.6e-126;  
 RESULT 675  
 ID ADN02731 standard; protein; 204 AA.  
 DE Human receptor and membrane -associated protein #34.  
 PN WO2004029218-A2.  
 PD 08-APR-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match 56.3%; Score 997.5; DB 8; Length 204;  
 Best Local Similarity 60.9%; Pred. No. 5.6e-88;  
 RESULT 676  
 ID ABG11697 standard; protein; 684 AA.  
 DE Novel human diagnostic protein #11688.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 52.7%; Score 933.5; DB 4; Length 684;  
 Best Local Similarity 64.9%; Pred. No. 5.3e-81;  
 RESULT 677  
 ID ABG12169 standard; protein; 684 AA.  
 DE Novel human diagnostic protein #12160.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 52.7%; Score 933.5; DB 4; Length 684;  
 Best Local Similarity 64.9%; Pred. No. 5.3e-81;  
 RESULT 678  
 ID ADR20055 standard; protein; 165 AA.  
 DE Human immune response associated protein (IRAP), seq id 15.  
 PN WO2004048550-A2.  
 PD 10-JUN-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match 36.9%; Score 653; DB 8; Length 165;  
 Best Local Similarity 90.9%; Pred. No. 1e-54;  
 RESULT 679  
 ID AAY12645 standard; protein; 124 AA.  
 DE Human 5' EST secreted protein SEQ ID NO: 310 from WO 9906553.  
 PN WO9906553-A2.  
 PD 11-FEB-1999.  
 PA (GEST ) GENSET.  
 Query Match 35.1%; Score 622; DB 2; Length 124;  
 Best Local Similarity 97.6%; Pred. No. 6.9e-52;  
 RESULT 680  
 ID AAW67811 standard; protein; 110 AA.  
 DE Human secreted protein encoded by gene 5 clone HASAV70.  
 PN WO9842738-A1.  
 PD 01-OCT-1998.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 32.8%; Score 582; DB 2; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-48;  
 RESULT 681  
 ID AAB32405 standard; protein; 110 AA.  
 DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:91.  
 PN WO200047602-A1.  
 PD 17-AUG-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 32.8%; Score 582; DB 3; Length 110;

Best Local Similarity 100.0%; Pred. No. 4.4e-48;  
RESULT 682  
ID ADAS7321 standard; protein; 110 AA.  
DE Human secreted protein #32.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.8%; Score 582; DB 6; Length 110;  
Best Local Similarity 100.0%; Pred. No. 4.4e-48;  
RESULT 683  
ID ADA56750 standard; protein; 110 AA.  
DE Human secreted protein #32.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.8%; Score 582; DB 6; Length 110;  
Best Local Similarity 100.0%; Pred. No. 4.4e-48;  
RESULT 684  
ID ADA40601 standard; protein; 110 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.8%; Score 582; DB 6; Length 110;  
Best Local Similarity 100.0%; Pred. No. 4.4e-48;  
RESULT 685  
ID ADA41198 standard; protein; 110 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.8%; Score 582; DB 6; Length 110;  
Best Local Similarity 100.0%; Pred. No. 4.4e-48;  
RESULT 686  
ID AAG00391 standard; protein; 97 AA.  
DE Human secreted protein, SEQ ID NO: 4472.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GSET) GENSET.  
Query Match 28.1%; Score 498; DB 3; Length 97;  
Best Local Similarity 100.0%; Pred. No. 5.1e-40;  
RESULT 687  
ID AAY11662 standard; protein; 98 AA.  
DE Human 5' EST secreted protein SEQ ID NO:314.  
PN WO9906439-A2.  
PD 11-FEB-1999.  
PA (GSET) GENSET.  
Query Match 28.1%; Score 498; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 5.2e-40;  
RESULT 688  
ID AM21122 standard; protein; 91 AA.  
DE Peptide #7556 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 26.6%; Score 471; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1.9e-37;  
RESULT 689  
ID ABA43438 standard; peptide; 91 AA.  
DE Peptide #10944 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 26.6%; Score 471; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1.9e-37;  
RESULT 690  
ID AAM37326 standard; protein; 91 AA.  
DE Peptide #11363 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 26.6%; Score 471; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1.9e-37;

RESULT 691  
ID ABB26408 standard; protein; 91 AA.  
DE Protein #8407 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 26.6%; Score 471; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1.9e-37;  
RESULT 692  
ID AAM77190 standard; protein; 91 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 37496.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 26.6%; Score 471; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1.9e-37;  
RESULT 693  
ID AAM64367 standard; protein; 91 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 36472.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 26.6%; Score 471; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1.9e-37;  
RESULT 694  
ID AAG58815 standard; peptide; 91 AA.  
DE Human liver peptide, SEQ ID NO 37463.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 26.6%; Score 471; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1.9e-37;  
RESULT 695  
ID AAG46203 standard; peptide; 91 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 35868.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 26.6%; Score 471; DB 5; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1.9e-37;  
RESULT 696  
ID AAB32404 standard; protein; 90 AA.  
DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:90.  
PN WO200047602-A1.  
PD 17-AUG-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 25.1%; Score 445; DB 3; Length 90;  
Best Local Similarity 100.0%; Pred. No. 6.3e-35;  
RESULT 697  
ID AAB47878 standard; protein; 328 AA.  
DE SCZ/CD84.  
PN WO200202054-A2.  
PD 10-JAN-2002.  
PA (RUTE) UNIV RUTGERS STATE NEW JERSEY.  
Query Match 20.5%; Score 362.5; DB 5; Length 328;  
Best Local Similarity 31.5%; Pred. No. 4.2e-26;  
RESULT 698  
ID AAE26238 standard; protein; 328 AA.  
DE Human CD84 protein.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 20.5%; Score 362.5; DB 5; Length 328;  
Best Local Similarity 31.5%; Pred. No. 4.2e-26;  
RESULT 699  
ID ADJ82907 standard; protein; 328 AA.  
DE Human PRO24934, SEQ ID 109.  
PN WO200402097-A2.  
PD 25-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 20.5%; Score 362.5; DB 8; Length 328;  
Best Local Similarity 31.5%; Pred. No. 4.2e-26;  
RESULT 700

ID ADO05708 standard; protein; 328 AA.  
DE Human leukocyte differentiation antigen CD84.  
PN WO2004032867-A2.  
PD 22-APR-2004.  
PA (TOLE-) TOLERRX INC.  
Query Match 20.5%; Score 362.5; DB 8; Length 328;  
Best Local Similarity 31.5%; Pred. No. 4.2e-26;  
RESULT 701  
ID ADQ19067 standard; protein; 328 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1886.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 20.5%; Score 362.5; DB 8; Length 328;  
Best Local Similarity 31.5%; Pred. No. 4.2e-26;  
RESULT 702  
ID ADP23943 standard; protein; 328 AA.  
DE PRO polypeptide SEQ ID NO:1121.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 20.5%; Score 362.5; DB 8; Length 328;  
Best Local Similarity 31.5%; Pred. No. 4.2e-26;  
RESULT 703  
ID AAU74891 standard; protein; 329 AA.  
DE Human secreted protein encoded by gene 164 clone HSAWF26.  
PN WO9839448-A2.  
PD 11-SEP-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 20.5%; Score 362.5; DB 2; Length 329;  
Best Local Similarity 31.5%; Pred. No. 4.2e-26;  
RESULT 704  
ID ABG95343 standard; protein; 329 AA.  
DE Human novel secreted protein #164.  
PN US6420526-B1.  
PD 16-JUL-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 20.5%; Score 362.5; DB 5; Length 329;  
Best Local Similarity 31.5%; Pred. No. 4.2e-26;  
RESULT 705  
ID AB034537 standard; protein; 329 AA.  
DE Region of human secreted protein encoded by cDNA sequence #164.  
PN US2003049618-A1.  
PD 13-MAR-2003.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D P.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN D R.  
PA (HUJJ/) HU J.  
PA (FLOR/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (FISC/) FISCHER C L.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (LAFI/) LAFLEUR D W.  
PA (LIYY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (KYAW/) KYAW H.  
Query Match 20.5%; Score 362.5; DB 6; Length 329;  
Best Local Similarity 31.5%; Pred. No. 4.2e-26;  
RESULT 706  
ID AD123198 standard; protein; 329 AA.

DE Novel human secreted protein seq id 483.  
PN US2003175858-A1.  
PD 18-SEP-2003.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D P.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN D R.  
PA (HUJJ/) HU J.  
PA (FLOR/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (FISC/) FISCHER C L.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (LAFI/) LAFLEUR D W.  
PA (LIYY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (KYAW/) KYAW H.  
Query Match 20.5%; Score 362.5; DB 7; Length 329;  
Best Local Similarity 31.5%; Pred. No. 4.2e-26;  
RESULT 707  
ID ADH74200 standard; protein; 329 AA.  
DE Human secreted protein #164.  
PN US2003225248-A1.  
PD 04-DEC-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 20.5%; Score 362.5; DB 8; Length 329;  
Best Local Similarity 31.5%; Pred. No. 4.2e-26;  
RESULT 708  
ID AAU74424 standard; protein; 629 AA.  
DE Mouse protein sequence #3, related to isolation of genes within SLE-1B.  
PN WO200188200-A2.  
PD 22-NOV-2001.  
PA (TEXA) UNIV TEXAS SYSTEM.  
Query Match 19.4%; Score 343; DB 5; Length 629;  
Best Local Similarity 29.3%; Pred. No. 8.4e-24;  
RESULT 709  
ID AAE26250 standard; protein; 289 AA.  
DE Human CD2001 protein #2.  
PN EPI223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.8%; Score 333.5; DB 5; Length 289;  
Best Local Similarity 31.0%; Pred. No. 2.2e-23;  
RESULT 710  
ID ABW01830 standard; protein; 289 AA.  
DE Human CD2001 protein #3.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.8%; Score 333.5; DB 7; Length 289;  
Best Local Similarity 31.0%; Pred. No. 2.2e-23;  
RESULT 711  
ID AAE12078 standard; protein; 289 AA.  
DE Dendritic cell (DC) DCLYR protein.  
PN WO200172773-A2.  
PD 04-OCT-2001.  
PA (NOVS) NOVARTIS AG.  
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
Query Match 18.7%; Score 330.5; DB 4; Length 289;  
Best Local Similarity 30.6%; Pred. No. 4.4e-23;  
RESULT 712  
ID AAE26243 standard; protein; 289 AA.

DE Human CD2001 protein.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.7%; Score 330.5; DB 5; Length 289;  
Best Local Similarity 30.6%; Pred. No. 4.4e-23;  
RESULT 713  
ID AAE26253 standard; protein; 289 AA.  
DE Human CD2001 protein #5.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.7%; Score 330.5; DB 5; Length 289;  
Best Local Similarity 30.6%; Pred. No. 4.4e-23;  
RESULT 714  
ID ABP65110 standard; protein; 289 AA.  
DE Hypoxia-induced protein #36.  
PN WO200246465-A2.  
PD 13-JUN-2002.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match 18.7%; Score 330.5; DB 5; Length 289;  
Best Local Similarity 30.6%; Pred. No. 4.4e-23;  
RESULT 715  
ID ABW01823 standard; protein; 289 AA.  
DE Human CD2001 protein #1.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.7%; Score 330.5; DB 7; Length 289;  
Best Local Similarity 30.6%; Pred. No. 4.4e-23;  
RESULT 716  
ID ABW01833 standard; protein; 289 AA.  
DE Human CD2001 protein #6.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.7%; Score 330.5; DB 7; Length 289;  
Best Local Similarity 30.6%; Pred. No. 4.4e-23;  
RESULT 717  
ID AAE26251 standard; protein; 289 AA.  
DE Human CD2001 protein #3.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.5%; Score 327.5; DB 5; Length 289;  
Best Local Similarity 30.3%; Pred. No. 8.6e-23;  
RESULT 718  
ID AAE26252 standard; protein; 289 AA.  
DE Human CD2001 protein #4.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.5%; Score 327.5; DB 5; Length 289;  
Best Local Similarity 30.3%; Pred. No. 8.6e-23;  
RESULT 719  
ID ABW01831 standard; protein; 289 AA.  
DE Human CD2001 protein #4.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.5%; Score 327.5; DB 7; Length 289;  
Best Local Similarity 30.3%; Pred. No. 8.6e-23;  
RESULT 720  
ID ABW01832 standard; protein; 289 AA.  
DE Human CD2001 protein #5.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.9%; Score 316.5; DB 7; Length 331;  
Best Local Similarity 29.6%; Pred. No. 1.2e-21;  
RESULT 721  
ID AAE26244 standard; protein; 270 AA.  
DE Human CD2001 mature protein.  
PN US2003180888-A1.

PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.5%; Score 327; DB 5; Length 270;  
Best Local Similarity 31.4%; Pred. No. 8.7e-23;  
RESULT 722  
ID ABW01824 standard; protein; 270 AA.  
DE Human CD2001 mature protein.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.5%; Score 327; DB 7; Length 270;  
Best Local Similarity 31.4%; Pred. No. 8.7e-23;  
RESULT 723  
ID AAE26239 standard; protein; 331 AA.  
DE Human CD2000 protein #3.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.0%; Score 319.5; DB 5; Length 331;  
Best Local Similarity 29.9%; Pred. No. 6.2e-22;  
RESULT 724  
ID ABW01818 standard; protein; 331 AA.  
DE Human CD2000 protein #2.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.0%; Score 319.5; DB 7; Length 331;  
Best Local Similarity 29.9%; Pred. No. 6.2e-22;  
RESULT 725  
ID ADL57103 standard; protein; 615 AA.  
DE Human NOV5a protein SEQ ID NO:48.  
PN WO2004022723-A2.  
PD 18-MAR-2004.  
PA (CURA-) CURAGEN CORP.  
Query Match 17.9%; Score 318; DB 8; Length 615;  
Best Local Similarity 30.3%; Pred. No. 2.2e-21;  
RESULT 726  
ID ADO63782 standard; protein; 654 AA.  
DE Human ly-9 polypeptide.  
PN US2004109862-A1.  
PD 10-JUN-2004.  
PA (EMTA/) EMTAGE P. C.  
Query Match 17.9%; Score 318; DB 8; Length 654;  
Best Local Similarity 30.3%; Pred. No. 2.4e-21;  
RESULT 727  
ID ADO78174 standard; protein; 654 AA.  
DE Human ly-9 polypeptide.  
PN US2004109863-A1.  
PD 10-JUN-2004.  
PA (EMTA/) EMTAGE P.  
Query Match 17.9%; Score 318; DB 8; Length 654;  
Best Local Similarity 30.3%; Pred. No. 2.4e-21;  
RESULT 728  
ID ADK41513 standard; protein; 331 AA.  
DE Anti-cell surface antigen related protein #1.  
PN WO2003068935-A2.  
PD 21-AUG-2003.  
PA (NUVE-) NUVELO INC.  
Query Match 17.9%; Score 316.5; DB 7; Length 331;  
Best Local Similarity 29.6%; Pred. No. 1.2e-21;  
RESULT 729  
ID AAE26222 standard; protein; 309 AA.  
DE Human CD2000 mature protein.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.8%; Score 315.5; DB 5; Length 309;  
Best Local Similarity 29.6%; Pred. No. 1.4e-21;  
RESULT 730  
ID ABW01801 standard; protein; 309 AA.  
DE Human CD2000 mature protein.  
PN US2003180888-A1.

PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.8%; Score 315.5; DB 7; Length 309;  
Best Local Similarity 29.6%; Pred. No. 1.4e-21;  
RESULT 731  
ID ABR90183 standard; protein; 331 AA.  
DE Human polypeptide SEQ ID NO 2559.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 17.8%; Score 315.5; DB 5; Length 331;  
Best Local Similarity 29.6%; Pred. No. 1.5e-21;  
RESULT 732  
ID AAE26220 standard; protein; 331 AA.  
DE Human CD2000 protein.  
PN EPI223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.8%; Score 315.5; DB 5; Length 331;  
Best Local Similarity 29.6%; Pred. No. 1.5e-21;  
RESULT 733  
ID ABR39107 standard; protein; 331 AA.  
DE Human NTB-A protein SEQ ID NO:2.  
PN WO2003008449-A1.  
PD 30-JAN-2003.  
PA (INNA-) INNATE PHARMA.  
PA (UTGE-) UNIV GENOVA.  
Query Match 17.8%; Score 315.5; DB 6; Length 331;  
Best Local Similarity 29.6%; Pred. No. 1.5e-21;  
RESULT 734  
ID AB003145 standard; protein; 331 AA.  
DE Human immunoglobulin (Ig) APEX4 protein.  
PN WO200277173-A2.  
PD 03-OCT-2002.  
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.  
Query Match 17.8%; Score 315.5; DB 6; Length 331;  
Best Local Similarity 29.6%; Pred. No. 1.5e-21;  
RESULT 735  
ID ADC52556 standard; protein; 331 AA.  
DE human dendritic cell membrane protein #SEQ ID 9.  
PN JP2003052374-A.  
PD 25-FEB-2003.  
PA (KIRI-) KIRIN BREWERY KK.  
Query Match 17.8%; Score 315.5; DB 7; Length 331;  
Best Local Similarity 29.6%; Pred. No. 1.5e-21;  
RESULT 736  
ID ABW01799 standard; protein; 331 AA.  
DE Human CD2000 protein #1.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.8%; Score 315.5; DB 7; Length 331;  
Best Local Similarity 29.6%; Pred. No. 1.5e-21;  
RESULT 737  
ID ADI37022 standard; protein; 331 AA.  
DE Novel human secreted and transmembrane protein PRO 71240.  
PN WO2004004649-A2.  
PD 15-JAN-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 17.8%; Score 315.5; DB 8; Length 331;  
Best Local Similarity 29.6%; Pred. No. 1.5e-21;  
RESULT 738  
ID AD066345 standard; protein; 331 AA.  
DE Novel human protein sequence #1318.  
PN EPI440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 17.8%; Score 315.5; DB 8; Length 331;  
Best Local Similarity 29.6%; Pred. No. 1.5e-21;  
RESULT 739  
ID AAU09868 standard; protein; 346 AA.  
DE Novel human secreted protein #9.  
PN WO200179454-A1.

PD 25-OCT-2001.  
PA (SMIK-) SMITHKLINE BEECHAM CORP.  
PA (SMIK-) SMITHKLINE BEECHAM PLC.  
Query Match 17.8%; Score 315.5; DB 5; Length 346;  
Best Local Similarity 29.6%; Pred. No. 1.6e-21;  
RESULT 740  
ID AAE26241 standard; protein; 331 AA.  
DE Human CD2000 protein #5.  
PN EPI223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.7%; Score 314.5; DB 5; Length 331;  
Best Local Similarity 29.6%; Pred. No. 1.9e-21;  
RESULT 741  
ID ABW01820 standard; protein; 331 AA.  
DE Human CD2000 protein #4.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.7%; Score 314.5; DB 7; Length 331;  
Best Local Similarity 29.6%; Pred. No. 1.9e-21;  
RESULT 742  
ID AAE26240 standard; protein; 331 AA.  
DE Human CD2000 protein #4.  
PN EPI223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.7%; Score 313.5; DB 5; Length 331;  
Best Local Similarity 29.6%; Pred. No. 2.4e-21;  
RESULT 743  
ID ABW01819 standard; protein; 331 AA.  
DE Human CD2000 protein #3.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.7%; Score 313.5; DB 7; Length 331;  
Best Local Similarity 29.6%; Pred. No. 2.4e-21;  
RESULT 744  
ID AAU74425 standard; protein; 610 AA.  
DE Human protein sequence #3, related to isolation of genes within SLE-1B.  
PN WO200188200-A2.  
PD 22-NOV-2001.  
PA (TEXA-) UNIV TEXAS SYSTEM.  
Query Match 17.6%; Score 312.5; DB 5; Length 610;  
Best Local Similarity 25.7%; Pred. No. 7.3e-21;  
RESULT 745  
ID AAE26242 standard; protein; 331 AA.  
DE Human CD2000 protein #6.  
PN EPI223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.6%; Score 311.5; DB 5; Length 331;  
Best Local Similarity 29.6%; Pred. No. 3.7e-21;  
RESULT 746  
ID ABW01821 standard; protein; 331 AA.  
DE Human CD2000 protein #5.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.6%; Score 311.5; DB 7; Length 331;  
Best Local Similarity 29.6%; Pred. No. 3.7e-21;  
RESULT 747  
ID AAG63166 standard; protein; 332 AA.  
DE Amino acid sequence of a CD84-like polypeptide.  
PN WO200155336-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 17.6%; Score 311; DB 4; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 748  
ID ASG96267 standard; protein; 332 AA.  
DE Human immunoglobulin superfamily protein IGSFP-5.  
PN WO200272794-A2.



PD 19-SEP-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 17.6%; Score 311; DB 5; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 749  
ID ABG34067 standard; protein; 332 AA.  
DE Human Pro peptide #38.  
PN WO200224888-A2.  
PD 28-MAR-2002.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 5; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 750  
ID ABU031170 standard; protein; 332 AA.  
DE Human immunoglobulin (Ig) APEX4v1 protein.  
PN WO200277173-A2.  
PD 03-OCT-2002.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 17.6%; Score 311; DB 6; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 751  
ID ADA37159 standard; protein; 332 AA.  
DE Human PRO20080 protein SEQ ID NO:2.  
PN WO2003055440-A2.  
PD 10-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 6; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 752  
ID ADA01344 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US200306879-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 6; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 753  
ID ADA43773 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003064474-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 6; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 754  
ID ADA43541 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003073196-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 6; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 755  
ID ADA01216 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003068782-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 6; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 756  
ID ADA01100 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003068780-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 757  
ID ADA43657 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003073190-A1.  
PD 17-APR-2003.

PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 758  
ID ADA06919 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003068781-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 759  
ID ADA08407 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003068783-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 760  
ID ADB99700 standard; protein; 332 AA.  
DE Human PRO polypeptide SEQ ID 76.  
PN US2003082728-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 761  
ID ADB86983 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003082726-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 762  
ID ADB66138 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003082729-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 763  
ID ADB99816 standard; protein; 332 AA.  
DE Human PRO polypeptide SEQ ID 76.  
PN US2003073192-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 764  
ID ADB99471 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003082731-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 765  
ID ADB66022 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003082732-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 766  
ID ADC23420 standard; protein; 332 AA.  
DE Human transmembrane PRO polypeptide (seqID 76).  
PN US2003073193-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.

Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 767  
ID ADF9429 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
FN US2003073194-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 768  
ID ADF04940 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003068778-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 769  
ID ADE11246 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003073191-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 770  
ID ADF8177 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003082733-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 771  
ID ADF95472 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
FN US2003064473-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 772  
ID ADF06402 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003073195-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 773  
ID ADE38177 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003119120-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 774  
ID ADF88293 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003073189-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 775  
ID ADF90874 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
FN US2003073188-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;

Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 776  
ID ADF9429 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
FN US2003078401-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 777  
ID ADF06522 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003077742-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 778  
ID ADF05473 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003077741-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 779  
ID ADF82474 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003077744-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 7; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 780  
ID ADE51727 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
FN US2003104560-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 781  
ID ADE51843 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
FN US2003104561-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 782  
ID ADE37701 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
FN US2003104564-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 783  
ID ADE37585 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
FN US2003104565-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 784  
ID ADF93536 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
FN US2003138901-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;

RESULT 785  
ID ADE52379 standard; protein; 332 AA.  
DE Human PRO20080.  
FN US200309661-A1.  
PD 29-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 786  
ID ADE38056 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003104566-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 787  
ID ADE76145 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003124665-A1.  
PD 03-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 788  
ID ADE39468 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003119117-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 789  
ID ADE04272 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003096364-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 790  
ID ADE39869 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003138896-A1.  
PD 24-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 791  
ID ADE19734 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003138903-A1.  
PD 24-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 792  
ID ADE77312 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
FN US2003124666-A1.  
PD 03-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 793  
ID ADE65420 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003119116-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 794  
ID ADE52379 standard; protein; 332 AA.  
DE Human PRO20080.  
FN US200309661-A1.  
PD 29-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 795  
ID ADE37940 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003119119-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 796  
ID ADE64550 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003119114-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 797  
ID ADE38985 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003096363-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 798  
ID ADE51959 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
FN US2003104562-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 799  
ID ADD09090 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
FN US2003138902-A1.  
PD 24-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 800  
ID ADE38769 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003108996-A1.  
PD 12-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 801  
ID ADE37469 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
FN US2003104563-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 802  
ID ADE06286 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
FN US2003138998-A1.  
PD 24-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 803  
ID ADD90145 standard; protein; 332 AA.

DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003138904-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 804  
ID ADE38653 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003119086-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 805  
ID ADE39584 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003119118-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 806  
ID ADE89189 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003138897-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 807  
ID ADE89956 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003138899-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 808  
ID ADE19850 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003138900-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 809  
ID ADE77428 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003124667-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 810  
ID ADE65304 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003119113-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 811  
ID ADE39352 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003119115-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 812  
ID ADE38537 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.

PN US2003104559-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 813  
ID ADG11090 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003170809-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 814  
ID ADG10974 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003077743-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 815  
ID ADH31502 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003119139-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 816  
ID ADH38750 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003119140-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 817  
ID ADH29385 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003119137-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 818  
ID ADH23688 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003119143-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 819  
ID ADH27018 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003119135-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 820  
ID ADH38286 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119124-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 821  
ID ADH26902 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003119134-A1.

PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 822  
ID ADH38170 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119123-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 823  
ID ADH3866 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003119141-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 824  
ID ADH3804 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003119142-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 825  
ID ADH40179 standard; protein; 332 AA.  
DE Human PRO20080 protein.  
PN US2003119132-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 826  
ID ADH40064 standard; protein; 332 AA.  
DE Human PRO20080 protein.  
PN US2003119133-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 827  
ID ADH31386 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003119138-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 828  
ID ADH29264 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003119136-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 829  
ID ADH49479 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119127-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 830  
ID ADH51943 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119125-A1.  
PD 26-JUN-2003.

PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 831  
ID ADH49798 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119128-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 832  
ID ADH52399 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119130-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 833  
ID ADH52515 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119129-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 834  
ID ADH58512 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119121-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 835  
ID ADH51827 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119126-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 836  
ID ADH58388 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119122-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 837  
ID ADI13585 standard; protein; 332 AA.  
DE Novel human secreted and transmembrane protein PRO20080.  
PN US2003119131-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 838  
ID ADK00841 standard; protein; 332 AA.  
DE Human PRO polypeptide #38.  
PN US2003186373-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 839  
ID ADL08582 standard; protein; 332 AA.  
DE Human secreted/transmembrane polypeptide PRO20080.  
PN US2003186372-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.

Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 840  
ID ADS10567 standard; protein; 332 AA.  
DE Human therapeutic protein - SEQ ID 804.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 17.6%; Score 311; DB 8; Length 332;  
Best Local Similarity 29.9%; Pred. No. 4.2e-21;  
RESULT 841  
ID AAE26249 standard; protein; 236 AA.  
DE Human CD2001 protein #1.  
PN EPI223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.0%; Score 301.5; DB 5; Length 236;  
Best Local Similarity 32.6%; Pred. No. 2.1e-20;  
RESULT 842  
ID ABW01829 standard; protein; 236 AA.  
DE Human CD2001 protein #2.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 17.0%; Score 301.5; DB 7; Length 236;  
Best Local Similarity 32.6%; Pred. No. 2.1e-20;  
RESULT 843  
ID AAE26246 standard; protein; 217 AA.  
DE Human CD2001 protein transmembrane domain.  
PN EPI223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 16.8%; Score 298; DB 5; Length 217;  
Best Local Similarity 33.8%; Pred. No. 4.1e-20;  
RESULT 844  
ID ABW01826 standard; protein; 217 AA.  
DE Human CD2001 protein extracellular domain.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 16.8%; Score 298; DB 7; Length 217;  
Best Local Similarity 33.8%; Pred. No. 4.1e-20;  
RESULT 845  
ID . ABG96270 standard; protein; 551 AA.  
DE Human immunoglobulin superfamily protein IGSFP-8.  
PN WO200272794-A2.  
PD 19-SEP-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 16.6%; Score 294.5; DB 5; Length 551;  
Best Local Similarity 30.4%; Pred. No. 3.5e-19;  
RESULT 846  
ID ADK98560 standard; protein; 565 AA.  
DE Human immune response associated protein IRAP-23 protein.  
PN WO2004020593-A2.  
PD 11-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 16.6%; Score 294.5; DB 8; Length 565;  
Best Local Similarity 30.4%; Pred. No. 3.6e-19;  
RESULT 847  
ID ADJ57243 standard; protein; 526 AA.  
DE Human NOV5c protein SEQ ID NO:188.  
PN WO2004022723-A2.  
PD 18-MAR-2004.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.9%; Score 282.5; DB 8; Length 526;  
Best Local Similarity 31.5%; Pred. No. 4.8e-18;  
RESULT 848  
ID ADJ57105 standard; protein; 526 AA.  
DE Human NOV5b protein SEQ ID NO:50.  
PN WO2004022723-A2.  
PD 18-MAR-2004.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.9%; Score 282.5; DB 8; Length 526;  
Best Local Similarity 31.5%; Pred. No. 4.8e-18;  
RESULT 849  
ID ADR20041 standard; protein; 91 AA.  
DE Human immune response associated protein (IRAP), seq id 1.  
PN WO2004048550-A2.  
PD 10-JUN-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 15.3%; Score 272; DB 8; Length 91;  
Best Local Similarity 100.0%; Pred. No. 3.8e-18;  
RESULT 850  
ID AAU08987 standard; protein; 220 AA.  
DE Novel human secreted protein #8.  
PN WO200179454-A1.  
PD 25-OCT-2001.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
Query Match 14.2%; Score 251; DB 5; Length 220;  
Best Local Similarity 35.4%; Pred. No. 1.5e-15;  
RESULT 851  
ID ABB53269 standard; protein; 310 AA.  
DE Human polypeptide #9.  
PN WO200181363-A1.  
PD 01-NOV-2001.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
Query Match 13.9%; Score 247; DB 5; Length 310;  
Best Local Similarity 26.7%; Pred. No. 6.1e-15;  
RESULT 852  
ID AAE26231 standard; protein; 195 AA.  
DE Human CD2000 protein #2.  
PN EPI223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 13.8%; Score 245; DB 5; Length 195;  
Best Local Similarity 35.1%; Pred. No. 4.8e-15;  
RESULT 853  
ID ABW01810 standard; protein; 195 AA.  
DE Human CD2000 protein extracellular domain #4.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 13.8%; Score 245; DB 7; Length 195;  
Best Local Similarity 35.1%; Pred. No. 4.8e-15;  
RESULT 854  
ID AAE26232 standard; protein; 203 AA.  
DE Human CD2000 protein transmembrane domain.  
PN EPI223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 13.8%; Score 245; DB 5; Length 203;  
Best Local Similarity 35.1%; Pred. No. 5.1e-15;  
RESULT 855  
ID ASW01811 standard; protein; 203 AA.  
DE Human CD2000 protein extracellular domain #5.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 13.8%; Score 245; DB 7; Length 203;  
Best Local Similarity 35.1%; Pred. No. 5.1e-15;  
RESULT 856  
ID ABB53268 standard; protein; 229 AA.  
DE Human polypeptide #8.  
PN WO200181363-A1.  
PD 01-NOV-2001.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
Query Match 13.3%; Score 236.5; DB 5; Length 229;  
Best Local Similarity 28.6%; Pred. No. 4.1e-14;  
RESULT 857  
ID AAB47322 standard; protein; 351 AA.  
DE APEX-2.  
PN WO200146260-A2.  
PD 28-JUN-2001.

PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 12.7%; Score 225.5; DB 4; Length 351;  
Best Local Similarity 26.0%; Pred. No. 8.8e-13;  
RESULT 858  
ID ABB89245 standard; protein; 168 AA.  
DE Human polypeptide SEQ ID NO 1621.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.4%; Score 219; DB 5; Length 169;  
Best Local Similarity 32.3%; Pred. No. 1.3e-12;  
RESULT 859  
ID ABU03171 standard; protein; 220 AA.  
DE Human immunoglobulin (Ig) APEX4sv1 protein.  
PN WO20027173-A2.  
PD 03-OCT-2002.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 11.6%; Score 206; DB 6; Length 220;  
Best Local Similarity 28.3%; Pred. No. 3.5e-11;  
RESULT 860  
ID AAE36225 standard; protein; 159 AA.  
DE Human CD2000 protein #1.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.3%; Score 200.5; DB 5; Length 159;  
Best Local Similarity 35.2%; Pred. No. 7.4e-11;  
RESULT 861  
ID ABW01804 standard; protein; 159 AA.  
DE Human CD2000 protein cytoplasmic domain #1.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.3%; Score 200.5; DB 7; Length 159;  
Best Local Similarity 35.2%; Pred. No. 7.4e-11;  
RESULT 862  
ID ABG96266 standard; protein; 221 AA.  
DE Human immunoglobulin superfamily protein IGSFP-4.  
PN WO200272794-A2.  
PD 19-SEP-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 11.3%; Score 199.5; DB 5; Length 221;  
Best Local Similarity 28.3%; Pred. No. 1.5e-10;  
RESULT 863  
ID ABM85690 standard; protein; 275 AA.  
DE Mouse protein sequence mCP1591.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.8%; Score 190.5; DB 7; Length 275;  
Best Local Similarity 29.1%; Pred. No. 1.5e-09;  
RESULT 864  
ID AAR97632 standard; protein; 343 AA.  
DE Mouse SLAMI T-cell co-stimulatory protein.  
PN WO9617060-A1.  
PD 06-JUN-1996.  
PA (SCHE-) SCHERING CORP.  
Query Match 10.5%; Score 186; DB 2; Length 343;  
Best Local Similarity 24.3%; Pred. No. 5.8e-09;  
RESULT 865  
ID AAR97628 standard; protein; 335 AA.  
DE Human SLAMI T-cell co-stimulatory protein.  
PN WO9617060-A1.  
PD 06-JUN-1996.  
PA (SCHE-) SCHERING CORP.  
Query Match 10.3%; Score 182.5; DB 2; Length 335;  
Best Local Similarity 22.5%; Pred. No. 1.2e-08;  
RESULT 866  
ID AAB71853 standard; protein; 335 AA.  
DE Human SLAM protein.  
PN WO200111046-A1.  
PD 15-FEB-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 10.3%; Score 182.5; DB 4; Length 335;  
Best Local Similarity 22.5%; Pred. No. 1.2e-08;  
RESULT 867  
ID AAU11927 standard; protein; 335 AA.  
DE Human protein sequence #1, related to isolation of genes within SLE-1B.  
PN WO200188200-A2.  
PD 22-NOV-2001.  
PA (TEXA-) UNIV TEXAS SYSTEM.  
Query Match 10.3%; Score 182.5; DB 5; Length 335;  
Best Local Similarity 22.5%; Pred. No. 1.2e-08;  
RESULT 868  
ID ABB90776 standard; protein; 335 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 285.  
PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO-) UNIV JOHNS HOPKINS.  
Query Match 10.3%; Score 182.5; DB 5; Length 335;  
Best Local Similarity 22.5%; Pred. No. 1.2e-08;  
RESULT 869  
ID ABUS4483 standard; protein; 335 AA.  
DE Human normal endothelial marker NEM 23.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO-) UNIV JOHNS HOPKINS.  
Query Match 10.3%; Score 182.5; DB 6; Length 335;  
Best Local Similarity 22.5%; Pred. No. 1.2e-08;  
RESULT 870  
ID ADL82887 standard; protein; 335 AA.  
DE Human PRO12612, SEQ ID 89.  
PN WO2004024097-A2.  
PD 25-MAR-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 10.3%; Score 182.5; DB 8; Length 335;  
Best Local Similarity 22.5%; Pred. No. 1.2e-08;  
RESULT 871  
ID ADP54607 standard; protein; 335 AA.  
DE Human PRO protein sequence SEQ ID NO:583.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 10.3%; Score 182.5; DB 8; Length 335;  
Best Local Similarity 22.5%; Pred. No. 1.2e-08;  
RESULT 872  
ID AAG77978 standard; protein; 334 AA.  
DE Human signalling lymphocytic activation molecule (SLAM)/SCZ.  
PN WO200180717-A2.  
PD 01-NOV-2001.  
PA (RUTG-) UNIV RUTGERS STATE NEW JERSEY.  
Query Match 10.2%; Score 181.5; DB 5; Length 334;  
Best Local Similarity 22.6%; Pred. No. 1.5e-08;  
RESULT 873  
ID AAR97631 standard; protein; 307 AA.  
DE Human SLAM4 T-cell co-stimulatory protein.  
PN WO9617060-A1.  
PD 06-JUN-1996.  
PA (SCHE-) SCHERING CORP.  
Query Match 10.2%; Score 180; DB 2; Length 307;  
Best Local Similarity 22.6%; Pred. No. 1.9e-08;  
RESULT 874  
ID AAY92181 standard; protein; 278 AA.  
DE Murine TANGO 195.  
PN WO200018800-A1.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 10.1%; Score 179; DB 3; Length 278;  
Best Local Similarity 25.9%; Pred. No. 2e-08;  
RESULT 875  
ID ABG74266 standard; protein; 278 AA.  
DE Human transmembrane protein TANGO 195 form 2.  
PN US2002155526-A1.  
PD 24-OCT-2002.  
PA (BUSF-) BUSFIELD S J.  
Query Match 10.1%; Score 179; DB 6; Length 278;

Best Local Similarity 25.9%; Pred. No. 2e-08;  
RESULT 876  
ID ABW01426 standard; protein; 278 AA.  
DE Murine TANGO 195 protein.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.1%; Score 179; DB 7; Length 278;  
Best Local Similarity 25.9%; Pred. No. 2e-08;  
RESULT 877  
ID ABW01428 standard; protein; 258 AA.  
DE Murine TANGO 195 mature protein.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.0%; Score 177.5; DB 7; Length 258;  
Best Local Similarity 27.0%; Pred. No. 2.5e-08;  
RESULT 878  
ID AAW67933 standard; protein; 33 AA.  
DE Fragment of human secreted protein encoded by gene 5.  
PN WO9842738-A1.  
PD 01-OCT-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 175; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 2.2e-09;  
RESULT 879  
ID ADS11838 standard; protein; 148 AA.  
DE Human therapeutic contig protein - SEQ ID 2075.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 9.6%; Score 170.5; DB 8; Length 148;  
Best Local Similarity 29.9%; Pred. No. 5.4e-08;  
RESULT 880  
ID AAY43138 standard; protein; 365 AA.  
DE Human NAIL protein sequence.  
PN WO9950297-A1.  
PD 07-OCT-1999.  
PA (IMNV-) IMMUNEX CORP.  
Query Match 9.6%; Score 170; DB 2; Length 365;  
Best Local Similarity 21.9%; Pred. No. 2.3e-07;  
RESULT 881  
ID AAM23942 standard; protein; 365 AA.  
DE Human EST encoded protein SEQ ID NO: 1467.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.6%; Score 170; DB 4; Length 365;  
Best Local Similarity 21.9%; Pred. No. 2.3e-07;  
RESULT 882  
ID AAU11929 standard; protein; 365 AA.  
DE Human protein sequence #2, related to isolation of genes within SLE-1B.  
PN WO200188200-A2.  
PD 22-NOV-2001.  
PA (TEXA-) UNIV TEXAS SYSTEM.  
Query Match 9.6%; Score 170; DB 5; Length 365;  
Best Local Similarity 21.9%; Pred. No. 2.3e-07;  
RESULT 883  
ID ADP56168 standard; protein; 365 AA.  
DE Human PRO protein sequence SEQ ID NO:2144.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 9.6%; Score 170; DB 8; Length 365;  
Best Local Similarity 21.9%; Pred. No. 2.3e-07;  
RESULT 884  
ID ADP25183 standard; protein; 365 AA.  
DE PRO polypeptide SEQ ID NO:2361.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 9.6%; Score 170; DB 8; Length 365;  
Best Local Similarity 21.9%; Pred. No. 2.3e-07;

RESULT 885  
ID ABP41447 standard; protein; 391 AA.  
DE Human ovarian antigen HWACN71, SEQ ID NO:2579.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 170; DB 5; Length 391;  
Best Local Similarity 21.9%; Pred. No. 2.5e-07;  
RESULT 886  
ID AAR97630 standard; protein; 305 AA.  
DE Human SLAM3 T-cell co-stimulatory protein.  
PN WO9617060-A1.  
PD 06-JUN-1996.  
PA (SCHE-) SCHERING CORP.  
Query Match 9.3%; Score 164.5; DB 2; Length 305;  
Best Local Similarity 21.7%; Pred. No. 5.9e-07;  
RESULT 887  
ID ABB90777 standard; protein; 305 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 286.  
PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO-) UNIV JOHNS HOPKINS.  
Query Match 9.3%; Score 164.5; DB 5; Length 305;  
Best Local Similarity 21.7%; Pred. No. 5.9e-07;  
RESULT 888  
ID ABU54484 standard; protein; 305 AA.  
DE Human normal endothelial marker NEM 23 secreted.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO-) UNIV JOHNS HOPKINS.  
Query Match 9.3%; Score 164.5; DB 6; Length 305;  
Best Local Similarity 21.7%; Pred. No. 5.9e-07;  
RESULT 889  
ID AAR97633 standard; protein; 329 AA.  
DE Mouse SLAM2 T-cell co-stimulatory protein.  
PN WO9617060-A1.  
PD 06-JUN-1996.  
PA (SCHE-) SCHERING CORP.  
Query Match 8.9%; Score 158.5; DB 2; Length 329;  
Best Local Similarity 27.0%; Pred. No. 2.5e-06;  
RESULT 890  
ID AAU11928 standard; protein; 329 AA.  
DE Mouse protein sequence #1, related to isolation of genes within SLE-1B.  
PN WO200188200-A2.  
PD 22-NOV-2001.  
PA (TEXA-) UNIV TEXAS SYSTEM.  
Query Match 8.9%; Score 158.5; DB 5; Length 329;  
Best Local Similarity 27.0%; Pred. No. 2.5e-06;  
RESULT 891  
ID AAR97629 standard; protein; 298 AA.  
DE Human SLAM2 T-cell co-stimulatory protein.  
PN WO9617060-A1.  
PD 06-JUN-1996.  
PA (SCHE-) SCHERING CORP.  
Query Match 8.6%; Score 152; DB 2; Length 298;  
Best Local Similarity 23.4%; Pred. No. 9.3e-06;  
RESULT 892  
ID ABB90778 standard; protein; 298 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 287.  
PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO-) UNIV JOHNS HOPKINS.  
Query Match 8.6%; Score 152; DB 5; Length 298;  
Best Local Similarity 23.4%; Pred. No. 9.3e-06;  
RESULT 893  
ID ABU54485 standard; protein; 298 AA.  
DE Human normal endothelial marker NEM 23 short.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO-) UNIV JOHNS HOPKINS.  
Query Match 8.6%; Score 152; DB 6; Length 298;  
Best Local Similarity 23.4%; Pred. No. 9.3e-06;  
RESULT 894



ID AAY52479 standard; protein; 285 AA.  
DE Human D-SLAM.  
PN WO940184-A1.  
PD 12-AUG-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 8.5%; Score 150.5; DB 3; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.2e-05;  
RESULT 895  
ID AAM93287 standard; protein; 285 AA.  
DE Human polypeptide, SEQ ID NO: 2773.  
PN EP130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 8.5%; Score 150.5; DB 4; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.2e-05;  
RESULT 896  
ID AAB71852 standard; protein; 285 AA.  
DE Human D-SLAM protein.  
PN WO200111046-A1.  
PD 15-FEB-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 8.5%; Score 150.5; DB 4; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.2e-05;  
RESULT 897  
ID AAB47323 standard; protein; 285 AA.  
DE APEX-3.  
PN WO200146260-A2.  
PD 28-JUN-2001.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 8.5%; Score 150.5; DB 4; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.2e-05;  
RESULT 898  
ID AAE12075 standard; protein; 285 AA.  
DE Dendritic cell (DC) DCIGR protein.  
PN WO200172773-A2.  
PD 04-OCT-2001.  
PA (NOVS) NOVARTIS AG.  
Query Match 8.5%; Score 150.5; DB 4; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.2e-05;  
RESULT 899  
ID ABG32412 standard; protein; 285 AA.  
DE Dendritic enriched secreted lymphocyte activation molecule (D-SLAM).  
PN WO200282955-A2.  
PD 15-AUG-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 8.5%; Score 150.5; DB 5; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.2e-05;  
RESULT 900  
ID ADC78929 standard; protein; 285 AA.  
DE Human PRO protein #79.  
PN WO2003034984-A2.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 8.5%; Score 150.5; DB 7; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.2e-05;  
RESULT 901  
ID ADD18914 standard; protein; 285 AA.  
DE Human disease related protein SeqID403.  
PN WO2003018621-A2.  
PD 06-MAR-2003.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match 8.5%; Score 150.5; DB 7; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.2e-05;  
RESULT 902  
ID ADF15146 standard; protein; 285 AA.  
DE Human albumin fusion protein-related protein SeqID444.  
PN WO2003060071-A2.  
PD 24-JUL-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 8.5%; Score 150.5; DB 7; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.2e-05;  
RESULT 903  
ID ADEL15146 standard; protein; 285 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3981.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 8.5%; Score 150.5; DB 8; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.2e-05;  
RESULT 904  
ID ADQ21161 standard; protein; 285 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3981.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 8.5%; Score 150.5; DB 8; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.2e-05;  
RESULT 905  
ID ADRI14157 standard; protein; 285 AA.  
DE Human NF-kappaB pathway-associated protein SeqID158.  
PN WO2004065577-A2.  
PD 05-AUG-2004.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 8.5%; Score 150.5; DB 8; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.2e-05;  
RESULT 906  
ID ADP25075 standard; protein; 285 AA.  
DE PRO polypeptide SEQ ID NO: 2253.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 8.5%; Score 150.5; DB 8; Length 285;  
Best Local Similarity 22.8%; Pred. No. 1.2e-05;  
RESULT 907  
ID ABW01429 standard; protein; 211 AA.  
DE Murine TANGO 195 protein extracellular domain.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 8.3%; Score 146.5; DB 7; Length 211;  
Best Local Similarity 28.6%; Pred. No. 1.9e-05;  
RESULT 908  
ID AAY92180 standard; protein; 312 AA.  
DE Partial human TANGO 195 protein.  
PN WO200018800-A1.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 8.2%; Score 146; DB 3; Length 312;  
Best Local Similarity 24.5%; Pred. No. 3.8e-05;  
RESULT 909  
ID ABG74265 standard; protein; 312 AA.  
DE Human transmembrane protein TANGO 195 form 1.  
PN US200215526-A1.  
PD 24-OCT-2002.  
PA (BUSF) BUSFIELD S J.  
Query Match 8.2%; Score 146; DB 6; Length 312;  
Best Local Similarity 24.5%; Pred. No. 3.8e-05;  
RESULT 910  
ID ABW01412 standard; protein; 312 AA.  
DE Human TANGO 195 form 1 protein.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 8.2%; Score 146; DB 7; Length 312;  
Best Local Similarity 24.5%; Pred. No. 3.8e-05;  
RESULT 911  
ID AAM24013 standard; protein; 318 AA.  
DE Human EST encoded protein SEQ ID NO: 1538.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 8.2%; Score 146; DB 4; Length 318;  
Best Local Similarity 24.5%; Pred. No. 3.9e-05;

ID ABG75377 standard; protein; 416 AA.  
 DE Human INSP052 complete protein.  
 PN WO2003093316-A2.  
 PD 13-NOV-2003.  
 PA (ARES-) ARES TRADING SA.  
 Query Match 8.0%; Score 142.5; DB 7; Length 416;  
 Best Local Similarity 22.1%; Pred. No. 0.00013;  
 RESULT 922  
 ID ADO47892 standard; protein; 416 AA.  
 DE Human protein SEQ ID NO:9.  
 PN WO2004007672-A2.  
 PD 22-JAN-2004.  
 PA (NUVE-) NUVELO INC.  
 Query Match 8.0%; Score 142.5; DB 8; Length 416;  
 Best Local Similarity 22.1%; Pred. No. 0.00013;  
 RESULT 923  
 ID ADS11056 standard; protein; 416 AA.  
 DE Human therapeutic protein - SEQ ID 1293.  
 PN WO2004080148-A2.  
 PD 23-SEP-2004.  
 PA (NUVE-) NUVELO INC.  
 Query Match 8.0%; Score 142.5; DB 8; Length 416;  
 Best Local Similarity 22.1%; Pred. No. 0.00013;  
 RESULT 924  
 ID ADQ65357 standard; protein; 367 AA.  
 DE Novel human protein sequence #330.  
 PN EP1440981-A2.  
 PD 28-JUL-2004.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Query Match 8.0%; Score 142; DB 8; Length 367;  
 Best Local Similarity 22.2%; Pred. No. 0.00012;  
 RESULT 925  
 ID ADA07622 standard; peptide; 149 AA.  
 DE Human secreted protein from gene 43, peptide #2.  
 PN US2003084412-A1.  
 PD 03-APR-2003.  
 PA (FISC/) FISCHER C L.  
 PA (ROSE/) ROSEN C A.  
 PA (SOPP/) SOPPET D R.  
 PA (RUBE/) RUBEN S M.  
 PA (KYAW/) KYAW H.  
 PA (LIYY/) LI Y.  
 PA (ZENG/) ZENG Z.  
 PA (LAPL/) LAFLEUR D W.  
 PA (MOOR/) MOORE P A.  
 PA (SHIY/) SHI Y.  
 PA (OLSE/) OLSEN H S.  
 PA (EBNE/) EBNER R.  
 PA (BREW/) BREWER L A.  
 Query Match 8.0%; Score 141; DB 7; Length 149;  
 Best Local Similarity 30.7%; Pred. No. 3.9e-05;  
 RESULT 926  
 ID ADN41449 standard; protein; 149 AA.  
 DE Novel human secreted protein fragment seqid 571.  
 PN US2004044191-A1.  
 PD 04-MAR-2004.  
 PA (FISC/) FISCHER C L.  
 PA (ROSE/) ROSEN C A.  
 PA (SOPP/) SOPPET D R.  
 PA (RUBE/) RUBEN S M.  
 PA (KYAW/) KYAW H.  
 PA (LIYY/) LI Y.  
 PA (ZENG/) ZENG Z.  
 PA (LAPL/) LAFLEUR D W.  
 PA (MOOR/) MOORE P A.  
 PA (SHIY/) SHI Y.  
 PA (OLSE/) OLSEN H.  
 PA (EBNE/) EBNER R.  
 PA (BIRS/) BIRSE C E.  
 Query Match 8.0%; Score 141; DB 8; Length 149;  
 Best Local Similarity 30.7%; Pred. No. 3.9e-05;  
 RESULT 927  
 ID ADA57556 standard; protein; 142 AA.

DE Human secreted protein #504.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.9%; Score 140.5; DB 6; Length 142;  
Best Local Similarity 31.0%; Pred. No. 4.1e-05;  
RESULT 928  
ID ADA41448 standard; protein; 142 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.9%; Score 140.5; DB 6; Length 142;  
Best Local Similarity 31.0%; Pred. No. 4.1e-05;  
RESULT 929  
ID ADC74567 standard; protein; 142 AA.  
DE Human secreted protein - SEQ ID 1200.  
PN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.9%; Score 140.5; DB 7; Length 142;  
Best Local Similarity 31.0%; Pred. No. 4.1e-05;  
RESULT 930  
ID ADD38086 standard; protein; 142 AA.  
DE Human secreted protein #269.  
PN WO200290526-A2.  
PD 14-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.9%; Score 140.5; DB 7; Length 142;  
Best Local Similarity 31.0%; Pred. No. 4.1e-05;  
RESULT 931  
ID ADN41130 standard; protein; 142 AA.  
DE Novel human secreted protein seqid 252.  
PN US2004044191-A1.  
PD 04-MAR-2004.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KIYAW/) KIYAW H.  
PA (LIYY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAFLEUR/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (OLSE/) OLSEN H.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.  
Query Match 7.9%; Score 140.5; DB 8; Length 142;  
Best Local Similarity 31.0%; Pred. No. 4.1e-05;  
RESULT 932  
ID AAY02692 standard; protein; 143 AA.  
DE Human secreted protein encoded by gene 43 clone HTADX17.  
PN WO9902546-A1.  
PD 21-JAN-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.9%; Score 140.5; DB 2; Length 143;  
Best Local Similarity 31.0%; Pred. No. 4.2e-05;  
RESULT 933  
ID ADA07371 standard; protein; 143 AA.  
DE Human secreted protein from gene 43.  
PN US2003064412-A1.  
PD 03-APR-2003.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KIYAW/) KIYAW H.  
PA (LIYY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAFLEUR/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (OLSE/) OLSEN H S.  
PA (EBNE/) EBNER R. A.  
PA (BREW/) BREWER L A.  
Query Match 7.9%; Score 140.5; DB 7; Length 143;  
Best Local Similarity 31.0%; Pred. No. 4.2e-05;  
RESULT 934  
ID ABW01419 standard; protein; 290 AA.  
DE Human TANGO 195 form 1 mature protein.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.9%; Score 140.5; DB 7; Length 290;  
Best Local Similarity 28.0%; Pred. No. 0.00012;  
RESULT 935  
ID ABW01438 standard; protein; 298 AA.  
DE Human TANGO 195 form 2 mature protein.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.9%; Score 140.5; DB 7; Length 298;  
Best Local Similarity 28.0%; Pred. No. 0.00012;  
RESULT 936  
ID AAG67932 standard; protein; 28 AA.  
DE Fragment of human secreted protein encoded by gene 5.  
PN WO9842738-A1.  
PD 01-OCT-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 139; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 5.3e-06;  
RESULT 937  
ID ABW01444 standard; protein; 263 AA.  
DE Human TANGO 195 mature protein.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.8%; Score 139; DB 7; Length 263;  
Best Local Similarity 24.3%; Pred. No. 0.00014;  
RESULT 938  
ID ABG75378 standard; protein; 418 AA.  
DE Murine INSP052 complete protein.  
PN WO2003093316-A2.  
PD 13-NOV-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 7.8%; Score 138.5; DB 7; Length 418;  
Best Local Similarity 22.9%; Pred. No. 0.00031;  
RESULT 939  
ID AAE26255 standard; protein; 70 AA.  
DE Human CD2001 protein Ig domain.  
PN EPI223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.8%; Score 138; DB 5; Length 70;  
Best Local Similarity 32.9%; Pred. No. 2.6e-05;  
RESULT 940  
ID ABW01835 standard; protein; 70 AA.  
DE Human CD2001 protein immunoglobulin (Ig) domain.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.8%; Score 138; DB 7; Length 70;  
Best Local Similarity 32.9%; Pred. No. 2.6e-05;  
RESULT 941  
ID ADO47895 standard; protein; 383 AA.  
DE Human mature protein SEQ ID NO:12.  
PN WO2004007672-A2.  
PD 22-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 7.8%; Score 137.5; DB 8; Length 383;  
Best Local Similarity 22.0%; Pred. No. 0.00034;  
RESULT 942  
ID ADM72195 standard; protein; 327 AA.  
DE Human CD2 amino acid sequence.  
PN WO2004022097-A1.

PD 18-MAR-2004.  
PA (MEDI-) MEDIMMUNE INC.  
Query Match 7.7%; Score 136.5; DB 8; Length 327;  
Best Local Similarity 23.9%; Pred. No. 0.00034;  
RESULT 943  
ID AAY813135 standard; protein; 351 AA.  
DE Human CD2.  
PN WO200012113-A2.  
PD 09-MAR-2000.  
PA (BIOJ) BIOGEN INC.  
Query Match 7.7%; Score 136.5; DB 3; Length 351;  
Best Local Similarity 23.9%; Pred. No. 0.00038;  
RESULT 944  
ID AAB61159 standard; protein; 351 AA.  
DE Human CD2.  
PN US6162432-A.  
PD 19-DEC-2000.  
PA (UNMI) UNIV MICHIGAN.  
PA (BIOJ) BIOGEN INC.  
Query Match 7.7%; Score 136.5; DB 4; Length 351;  
Best Local Similarity 23.9%; Pred. No. 0.00038;  
RESULT 945  
ID ABB81993 standard; protein; 351 AA.  
DE Human CD2 polypeptide.  
PN WO200260480-A1.  
PD 08-AUG-2002.  
PA (BIOJ) BIOGEN INC.  
Query Match 7.7%; Score 136.5; DB 5; Length 351;  
Best Local Similarity 23.9%; Pred. No. 0.00038;  
RESULT 946  
ID AAU76227 standard; protein; 351 AA.  
DE Mammalian CD2 antigen protein.  
PN US2002009449-A1.  
PD 24-JAN-2002.  
PA (BIOJ) BIOGEN INC.  
Query Match 7.7%; Score 136.5; DB 5; Length 351;  
Best Local Similarity 23.9%; Pred. No. 0.00038;  
RESULT 947  
ID ABM85811 standard; protein; 351 AA.  
DE Human protein sequence HCP48906.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 7.7%; Score 136.5; DB 7; Length 351;  
Best Local Similarity 23.9%; Pred. No. 0.00038;  
RESULT 948  
ID ADQ60208 standard; protein; 351 AA.  
DE Human CD2 protein.  
PN US2004136987-A1.  
PD 15-JUL-2004.  
PA (BIOJ) BIOGEN INC.  
PA (UNMI) UNIV MICHIGAN.  
Query Match 7.7%; Score 136.5; DB 8; Length 351;  
Best Local Similarity 23.9%; Pred. No. 0.00038;  
RESULT 949  
ID AAR06365 standard; protein; 353 AA.  
DE Soluble two domain human CD2 glycoprotein.  
PN WO9008187-A.  
PD 26-JUL-1990.  
PA (DAND) DANA FARBER CANCER INST INC.  
Query Match 7.7%; Score 136.5; DB 2; Length 353;  
Best Local Similarity 23.9%; Pred. No. 0.00038;  
RESULT 950  
ID AAU29274 standard; protein; 198 AA.  
DE Human PRO polypeptide sequence #251.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 4; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 951  
ID ABUS8650 standard; protein; 198 AA.

DE Human PRO polypeptide #251.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 952  
ID ABUS88198 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 953  
ID ABUS4513 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 954  
ID ABR66387 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 955  
ID ABR65777 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 956  
ID ABUS9717 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 957  
ID ABUS2956 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 958  
ID ABUS0077 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 959  
ID ABR68326 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 960  
ID ABUS6379 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 961  
ID ABUS2810 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003036149-A1.  
PD 20-FEB-2003.

Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 962  
ID ABO08887 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 963  
ID ABO2939 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 964  
ID ABR75093 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 965  
ID ABR94855 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 966  
ID ABUS828 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 967  
ID ABUS988 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 968  
ID ABUS8203 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 969  
ID ABUS1909 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 970  
ID ABUS9602 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 971  
ID ABUS6443 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match

Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 972  
ID ABUS67656 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 973  
ID ABUS0684 standard; protein; 198 AA.  
DE Human PRO protein #251.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 974  
ID ABR99602 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 975  
ID ABR98992 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 976  
ID ABO16515 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 977  
ID ABR92415 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 978  
ID ABO19056 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 979  
ID ABR78477 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 980  
ID ABUS5213 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 981  
ID ABO0352 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match

Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 982  
ID ABO11684 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 983  
ID ABO02329 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 984  
ID AB08359 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
FN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 985  
ID AB08359 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 986  
ID ABO06399 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
FN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 987  
ID ABR59435 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 988  
ID ABO09497 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 989  
ID ABO19361 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
FN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 990  
ID ABO11379 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 991  
ID ABR66997 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 992

ID ABO16210 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 993  
ID ABO13916 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 994  
ID AB065819 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein, SEQ ID 502.  
FN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 995  
ID ABO07667 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
FN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 996  
ID ABO03854 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 997  
ID ABR67302 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 998  
ID ABO15905 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 999  
ID AB056186 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein, PRO4421.  
FN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1000  
ID AB065514 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
FN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1001  
ID AB095459 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
FN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1002  
ID AB071362 standard; protein; 198 AA.  
DE Human PRO4421 protein.

PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1003  
ID ABO077972 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1004  
ID ABR70213 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1005  
ID ABR69546 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1006  
ID ABO01687 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1007  
ID ABU81489 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1008  
ID ABR60286 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1009  
ID ABR68021 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1010  
ID ABR65409 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1011  
ID ABR68631 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1012  
ID ABR72043 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032135-A1.

PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1013  
ID ABUS523 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1014  
ID ABUS9213 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1015  
ID ABUS3293 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1016  
ID ABUS95149 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1017  
ID ABUS0697 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1018  
ID ABUS4208 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1019  
ID ABUS3859 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1020  
ID ABR65104 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1021  
ID ABR68936 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1022  
ID ABO06752 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003036125-A1.  
PD 20-FEB-2003.

Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1023  
ID ABR99297 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
DE Human PRO polypeptide #251.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US20030316136-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
DE Human PRO polypeptide #251.  
PN US20030316138-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
DE ABO08277 standard; protein; 198 AA.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032120-A1.  
PD 13-FEB-2003.

ID ABU94169 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032155-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1034  
ID ABO00042 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1035  
ID ABR66692 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1036  
ID ABR91110 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1037  
ID ABU94537 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1038  
ID ABU79419 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1039  
ID ABU86748 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1040  
ID ABU87053 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1041  
ID ABU94842 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1042  
ID ABO04769 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1043  
ID ABR70518 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.



PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1044  
ID ABR66082 standard; protein; 198 AA.  
DE Human secreted polypeptide #251.  
PN US20030322301-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1045  
ID ABR66082 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US200303165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1046  
ID ABR64799 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1047  
ID ABR79724 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1048  
ID ABR93115 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US200303142-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1049  
ID ABR96074 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1050  
ID ABR91294 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1051  
ID ABR90387 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1052  
ID ABR09802 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1053  
ID ABR011074 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003036150-A1.  
PD 20-FEB-2003.

Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1054  
ID ABR71128 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1055  
ID ABR87736 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1056  
ID ABR91604 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1057  
ID ABR84818 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1058  
ID ABR69908 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1059  
ID ABR80285 standard; protein; 198 AA.  
DE Human PRO protein #251.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1060  
ID ABR93554 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1061  
ID ABR010107 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1062  
ID ABR009192 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1063  
ID ABR10760 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein #251.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;

RESULT 1064  
ID ABU95769 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1065  
ID ABU96978 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1066  
ID ABR70823 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1067  
ID ABO05174 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1068  
ID ABO08582 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1069  
ID ABO05789 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1070  
ID ABR74178 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1071  
ID ABR95770 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1072  
ID ABR81067 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1073  
ID ABR81372 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;

Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1074  
ID ABO01068 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1075  
ID ABR88670 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1076  
ID ABR77491 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1077  
ID ABO28975 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1078  
ID ABO31720 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1079  
ID ABO08137 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1080  
ID ABO40617 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1081  
ID ABO36042 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1082  
ID ABO44181 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;

Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1083  
ID ADA78254 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1084  
ID ABM24976 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1085  
ID ABO3244 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003036131-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1086  
ID ABR90500 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003040075-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1087  
ID ABM17414 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1088  
ID ABR95160 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003044930-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1089  
ID ABR95465 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1090  
ID ABO21703 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1091  
ID ABR97967 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1092  
ID ABR87755 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003068705-A1.  
PA (GETH ) GENENTECH INC.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1093  
ID ABM77796 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1094  
ID ABM28026 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1095  
ID ABM06307 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1096  
ID ABM03813 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1097  
ID ABM35264 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1098  
ID ABM26501 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1099  
ID ABO48283 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1100  
ID ABR93025 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
FN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1101  
ID ABO24786 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
FN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1102  
ID ABM11797 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1103  
ID ABM02898 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1104  
ID ABM16194 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1105  
ID ABO27755 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1106  
ID ABM29246 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1107  
ID ABM07222 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1108  
ID ABM21316 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1109  
ID ABM09662 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1110  
ID ABO41532 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1111  
ID ABO36347 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1111  
ID ABO36347 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1112  
ID ABO43876 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1113  
ID ABM76576 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1114  
ID ABM76272 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1115  
ID ABM25891 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1116  
ID ABM26196 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1117  
ID ABO03549 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1118  
ID ABO02634 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1119  
ID ABR90805 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1120  
ID ABR73873 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1121  
ID ABO17125 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1122  
ID ABR94550 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1123  
ID ABR76057 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1124  
ID ABR71433 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1125  
ID ABR93330 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1126  
ID ABR93635 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1127  
ID ABR88060 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1128  
ID ABO28060 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1129  
ID ABO30195 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1130  
ID ABO52553 standard; protein; 198 AA.

ID ABO33404 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1131  
ID ABM05092 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1132  
ID ABM09052 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1133  
ID ABO36652 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1134  
ID ABO35737 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1135  
ID ABO39702 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1136  
ID ABM10577 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1137  
ID ABM12102 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1138  
ID ABO52248 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
RESULT 1139  
ID ABO52553 standard; protein; 198 AA.

```
DE Human PRO polypeptide #251.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1140
ID ABO23871 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1141
ID ABR97357 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1142
ID ABR97145 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1143
ID ABM1187 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1144
ID ABM2831 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1145
ID ABO22330 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1146
ID ABM15457 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1147
ID ABM06612 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1148
ID ABM04423 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1149
ID ABM22536 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1150
ID ABM07832 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1151
ID ABO40922 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1152
ID ABM35569 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1153
ID ABM33332 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1154
ID ABO52858 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1155
ID ABO50418 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1156
ID ABU99412 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1157
ID ABO04464 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
```

RESULT 1158  
ID ABM18634 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US200305480-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1159  
ID ABR97662 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1160  
ID ABR80762 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1161  
ID ABM01373 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1162  
ID ABR88975 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073169-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1163  
ID ABM13627 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1164  
ID ABM21011 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1165  
ID ABO42142 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1166  
ID ABO42752 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1167  
ID ABM10272 standard; protein; 198 AA.

DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1168  
ID ABO38787 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1169  
ID ABM33027 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1170  
ID ABM22841 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1171  
ID ABM75052 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1172  
ID ADA80046 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003073173-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1173  
ID ABR96442 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1174  
ID ABM02593 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1175  
ID ABR86535 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1176  
ID ABR86840 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;

Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1177  
ID ABM16804 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064448-A1.  
PA (GETH ) GENENTECH INC.  
PD 03-APR-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1178  
ID ABM29856 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064456-A1.  
PA (GETH ) GENENTECH INC.  
PD 03-APR-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1179  
ID ABO29280 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1180  
ID ABM24061 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1181  
ID ABM23451 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1182  
ID ABM22231 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1183  
ID ABO37872 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1184  
ID ABM28636 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1185  
ID ABM28941 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1186  
ID ABM66585 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049763-A1.  
PD 13-MAR-2003.

DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068737-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1187  
ID ABM75967 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1188  
ID ABM34247 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1189  
ID ABM34552 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1190  
ID ABO20483 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1191  
ID ABO21398 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1192  
ID ABO22313 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1193  
ID ABR96747 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1194  
ID ABR85925 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1195  
ID ABR9907 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049763-A1.  
PD 13-MAR-2003.



PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1196  
ID ABM00458 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1197  
ID ABM00763 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1198  
ID ABO29890 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1199  
ID ABM23756 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1200  
ID ABM29551 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1201  
ID ABO38482 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1202  
ID ABO45782 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1203  
ID ABM20706 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1204  
ID ADA81773 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;

RESULT 1205  
ID ABO16820 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1206  
ID ABO18446 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1207  
ID ABO22873 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1208  
ID ABO23178 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1209  
ID ABR92720 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1210  
ID ABR81677 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1211  
ID ABM78101 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1212  
ID ABR89890 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1213  
ID ABM26806 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;  
Pred. No. 0.00026;  
RESULT 1214  
ID ABM13932 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1215  
ID ABO28670 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1216  
ID ABO30500 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1217  
ID ABO07527 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1218  
ID ABO04118 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1219  
ID ABO37262 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1220  
ID ABO41837 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1221  
ID ABO35432 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1222  
ID ABO25281 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1223  
ID ABO47673 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;

RESULT 1224  
ID ABO47978 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1225  
ID ABO48588 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1226  
ID ABO51638 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1227  
ID ABO51943 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1228  
ID ABO50723 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1229  
ID ABR79847 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1230  
ID ABO17109 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1231  
ID ABO18141 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1232  
ID ABO21093 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1233  
ID ABR97052 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054462-A1.

PA 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1234  
ID ABM12407 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1235  
ID ABM16499 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1236  
ID ABM24366 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064441-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1237  
ID ABM14847 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1238  
ID ABM04728 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1239  
ID ABM06917 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1240  
ID ABM09357 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073174-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1241  
ID ABO39397 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1242  
ID ABM75662 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;  
Query Match

Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1243  
ID ABM25586 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1244  
ID ABM20096 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1245  
ID ABO47002 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1246  
ID ABO47307 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1247  
ID ADA83571 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1248  
ID ABR71738 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1249  
ID ABR72348 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1250  
ID ABR98687 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1251  
ID ABO07057 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1252  
ID ABR85010 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040057-A1.  
PD 27-FEB-2003.

```
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1253
ID ABR73568 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1254
ID ABR7662 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US200304932-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1255
ID ABR73263 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1256
ID ABM18329 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1257
ID ABO20788 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1258
ID ABO25531 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1259
ID ABO25836 standard; protein; 198 AA.
DE Human secreted polypeptide #251.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1260
ID ABR94245 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1261
ID ABR80152 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1262
ID ABM11492 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049748-A1.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1263
ID ABO33099 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1264
ID ABO30805 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1265
ID ABO31110 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1266
ID ABM27416 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1267
ID ABM30161 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1268
ID ABM05697 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1269
ID ABM15762 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1270
ID ABM08747 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1271
ID ABO42447 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049748-A1.
```

PD 13-MAR-2003.  
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;  
Query Match 30.7%; Pred. No. 0.00026;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1272  
ID ABO38177 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003058765-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1273  
ID ABO46087 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1274  
ID ABO66890 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1275  
ID ADB20614 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1276  
ID ABM19791 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1277  
ID ABO49503 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1278  
ID ABO49808 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1279  
ID ADA78866 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1280  
ID ABR88365 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.

Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1281  
ID ABM27111 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1282  
ID ABM03508 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1283  
ID ABO40007 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 6; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1284  
ID ABO50113 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1285  
ID ABO51028 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1286  
ID ABO05484 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1287  
ID ABR74788 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049924-A1.  
PD 06-MAR-2003.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1288  
ID ABR77267 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049927-A1.  
PD 06-MAR-2003.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1289  
ID ABM18024 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1290  
ID ABR96075 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.

PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1291  
ID ABO22008 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1292  
ID ABO20178 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1293  
ID ABO24481 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1294  
ID ABR66230 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1295  
ID ABM1082 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1296  
ID ABM76881 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1297  
ID ABR89585 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1298  
ID ABM12712 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1299  
ID ABM06002 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1300  
ID ABO35127 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1301  
ID ABM03203 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1302  
ID ABM19181 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1303  
ID ABM19486 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1304  
ID ABO46697 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1305  
ID ABO49198 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1306  
ID ABR69241 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1307  
ID ABR89280 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1308  
ID ABR72653 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1309  
ID ABR74483 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.

PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;  
Query Match  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1310  
ID ABO18751 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1311  
ID ABR80457 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;  
Query Match  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1312  
ID ABO1678 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;  
Query Match  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1313  
ID ABO2288 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;  
Query Match  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1314  
ID ABR87450 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;  
Query Match  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1315  
ID ABR13017 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;  
Query Match  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1316  
ID ABR30771 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;  
Query Match  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1317  
ID ABR24671 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;  
Query Match  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1318  
ID ABO29585 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068697-A1.  
PD 10-APR-2003.

PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;  
Query Match  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1319  
ID ABO31415 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;  
Query Match  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1320  
ID ABR14542 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;  
Query Match  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1321  
ID ABO0967 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;  
Query Match  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1322  
ID ABO39092 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;  
Query Match  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1323  
ID ABR34857 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1324  
ID ABO51333 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;  
Query Match  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1325  
ID ABO04159 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1326  
ID ABO10629 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1327  
ID ABR77872 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
RESULT 1328  
ID ABR79082 standard; protein; 198 AA.

DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1329  
ID ABO24176 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1330  
ID ABR93940 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1331  
ID ABO401983 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1332  
ID ABO401983 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1333  
ID ABR90195 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1334  
ID ABR27721 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1335  
ID ABR13322 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1336  
ID ABO32025 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1337  
ID ABR14237 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068683-A1.

PD 10-APR-2003.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1338  
ID ABO8442 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1339  
ID ABO40312 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068681-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1340  
ID ABO40312 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1341  
ID ABO40312 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1342  
ID ABO40312 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1343  
ID ABO48893 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1344  
ID ABR72958 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1345  
ID ABO15600 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1346  
ID ABR85315 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1347



ID ABO15295 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1348  
ID ABO17430 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1349  
ID ABM17719 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1350  
ID ABR85620 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1351  
ID ABM77186 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1352  
ID ABO28365 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1353  
ID ABM23146 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1354  
ID ABM30466 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1355  
ID ABM21926 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1356  
ID ABM21621 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1357  
ID ABM15152 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1358  
ID ABO41227 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1359  
ID ABO36957 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1360  
ID ABO37567 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1361  
ID ABM75357 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1362  
ID ABM33637 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1363  
ID ABO46392 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1364  
ID ADA82937 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1365  
ID ABM31991 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068680-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;  
RESULT 1366  
ID ABM31991 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068680-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;  
Pred. No. 0.00026;

Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1366  
ID ABM31381 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1367  
ID ADB66245 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1368  
ID ABM32296 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1369  
ID ABM32601 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1370  
ID ABM31686 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1371  
ID ABM31076 standard; protein; 198 AA.  
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1372  
ID ADD05975 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1373  
ID ADG02970 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US200307397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1374  
ID ADG01677 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US200307399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1375  
ID ADF95852 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1376  
ID ADG12667 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1377  
ID ADH09327 standard; protein; 198 AA.  
DE Human PRO polypeptide #251.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1378  
ID ADL33106 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1379  
ID ADM30642 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 7; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1380  
ID ADE74639 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 8; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1381  
ID ADE75251 standard; protein; 198 AA.  
DE Human secreted/transmembrane protein (PRO) #251.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 8; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1382  
ID ADF96464 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 8; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1383  
ID ADG04735 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 134.5; DB 8; Length 198;  
Best Local Similarity 30.7%; Pred. No. 0.00026;  
RESULT 1384  
ID ADG00895 standard; protein; 198 AA.  
DE Novel human secreted and transmembrane protein PRO4421.  
PN US2003215911-A1.  
PD 20-NOV-2003.

PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 8; Length 198;  
 Query Match Best Local Similarity 30.7%; Pred. No. 0.00026;  
 RESULT 1385  
 ID ADEG3380 standard; protein; 198 AA.  
 DE Human PRO polypeptide #251.  
 PN US2003215910-A1.  
 PD 20-NOV-2003.  
 PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 8; Length 198;  
 Query Match Best Local Similarity 30.7%; Pred. No. 0.00026;  
 RESULT 1386  
 ID ADH26432 standard; protein; 198 AA.  
 DE Novel human secreted and transmembrane protein PRO4421.  
 PN US2003068770-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 8; Length 198;  
 Query Match Best Local Similarity 30.7%; Pred. No. 0.00026;  
 RESULT 1387  
 ID ADH33401 standard; protein; 198 AA.  
 DE Human PRO polypeptide #251.  
 PN US2003068768-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 8; Length 198;  
 Query Match Best Local Similarity 30.7%; Pred. No. 0.00026;  
 RESULT 1388  
 ID ADJ55140 standard; protein; 198 AA.  
 DE Human PRO polypeptide #251.  
 PN US2004023321-A1.  
 PD 05-FEB-2004.  
 PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 8; Length 198;  
 Query Match Best Local Similarity 30.7%; Pred. No. 0.00026;  
 RESULT 1389  
 ID ADJ64911 standard; protein; 198 AA.  
 DE Human PRO polypeptide #251.  
 PN US2004038337-A1.  
 PD 26-FEB-2004.  
 PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 8; Length 198;  
 Query Match Best Local Similarity 30.7%; Pred. No. 0.00026;  
 RESULT 1390  
 ID ADMJ1807 standard; protein; 198 AA.  
 DE Novel human secreted and transmembrane protein PRO4421.  
 PN US2004048334-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 8; Length 198;  
 Query Match Best Local Similarity 30.7%; Pred. No. 0.00026;  
 RESULT 1391  
 ID ADM36854 standard; protein; 198 AA.  
 DE Novel human secreted and transmembrane protein PRO4421.  
 PN US2004053358-A1.  
 PD 18-MAR-2004.  
 PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 8; Length 198;  
 Query Match Best Local Similarity 30.7%; Pred. No. 0.00026;  
 RESULT 1392  
 ID ADM40659 standard; protein; 198 AA.  
 DE Novel human secreted and transmembrane protein PRO4421.  
 PN US2004048335-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 8; Length 198;  
 Query Match Best Local Similarity 30.7%; Pred. No. 0.00026;  
 RESULT 1393  
 ID ADN38267 standard; protein; 198 AA.  
 DE Novel human secreted and transmembrane protein PRO4421.  
 PN US2004091959-A1.  
 PD 13-MAY-2004.  
 PA (GETH ) GENENTECH INC. 7.6%; Score 134.5; DB 8; Length 198;  
 Query Match Best Local Similarity 30.7%; Pred. No. 0.00026;  
 RESULT 1394  
 ID ADEG3380 standard; protein; 240 AA.  
 DE Rat Protein P10252, SEQ ID NO 9319.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO ) GEN HOSPITAL CORP. 7.6%; Score 134.5; DB 8; Length 198;  
 Query Match Best Local Similarity 30.7%; Pred. No. 0.00026;  
 RESULT 1395  
 ID AAR74221 standard; protein; 332 AA.  
 DE Epitope on the primary CD2 sequence.  
 PN US5411861-A.  
 PD 02-MAY-1995.  
 PA (GEHO ) GEN HOSPITAL CORP. 7.6%; Score 134.5; DB 8; Length 198;  
 Query Match Best Local Similarity 30.7%; Pred. No. 0.00026;  
 RESULT 1396  
 ID AAY30457 standard; protein; 332 AA.  
 DE Predicted sequence of the mature CD2 protein.  
 PN US5955264-A.  
 PD 21-SEP-1999.  
 PA (GEHO ) GEN HOSPITAL CORP. 7.6%; Score 134.5; DB 8; Length 198;  
 Query Match Best Local Similarity 30.7%; Pred. No. 0.00026;  
 RESULT 1397  
 ID ADA25185 standard; protein; 332 AA.  
 DE Mature CD2 protein.  
 PN US6579676-B1.  
 PD 17-JUN-2003.  
 PA (GEHO ) GEN HOSPITAL CORP. 7.6%; Score 134.5; DB 8; Length 198;  
 Query Match Best Local Similarity 30.7%; Pred. No. 0.00026;  
 RESULT 1398  
 ID AAR11921 standard; protein; 351 AA.  
 DE Human T11 sugar protein.  
 PN JP03035782-A.  
 PD 15-FEB-1991.  
 PA (DAND ) DANA FARBER CANCER INST INC. 7.5%; Score 133.5; DB 2; Length 351;  
 Query Match Best Local Similarity 24.4%; Pred. No. 0.00074;  
 RESULT 1399  
 ID AAR20803 standard; protein; 351 AA.  
 DE Human CD2 antigen.  
 PN WO9201049-A.  
 PD 23-JAN-1992.  
 PA (GEHO ) GEN HOSPITAL CORP. 7.5%; Score 133.5; DB 2; Length 351;  
 Query Match Best Local Similarity 22.7%; Pred. No. 0.00074;  
 RESULT 1400  
 ID AAR34223 standard; protein; 351 AA.  
 DE Amino acid sequence of CD2.  
 PN WO9306852-A2.  
 PD 15-APR-1993.  
 PA (BIOJ ) BIOGEN INC. 7.5%; Score 133.5; DB 2; Length 351;  
 Query Match Best Local Similarity 23.6%; Pred. No. 0.00074;  
 RESULT 1401  
 ID AAR91431 standard; protein; 351 AA.  
 DE Human CD2.  
 PN US5506126-A.  
 PD 09-APR-1996.  
 PA (GEHO ) GEN HOSPITAL CORP. 7.5%; Score 133.5; DB 2; Length 351;  
 Query Match Best Local Similarity 22.7%; Pred. No. 0.00074;  
 RESULT 1402  
 ID AAW80440 standard; protein; 351 AA.  
 DE Human CD2 antigen.  
 PN US5830731-A.  
 PD 03-NOV-1998.  
 PA (GEHO ) GEN HOSPITAL CORP. 7.5%; Score 133.5; DB 2; Length 351;

Query Match 7.5%; Score 133.5; DB 2; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00074;  
RESULT 1403  
ID AA086188 standard; protein; 351 AA.  
DE Human CD2 antigen.  
PN US5849898-A.  
PD 15-DEC-1998.  
PA (GENE) GEN HOSPITAL CORP.  
Query Match 7.5%; Score 133.5; DB 2; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00074;  
RESULT 1404  
ID AAY96126 standard; protein; 351 AA.  
DE Human cell surface antigen CD2.  
PN US6111093-A.  
PD 29-AUG-2000.  
PA (GENE) GEN HOSPITAL CORP.  
Query Match 7.5%; Score 133.5; DB 3; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00074;  
RESULT 1405  
ID AAU02435 standard; protein; 351 AA.  
DE Human lymphocyte cell surface antigen CD2 polypeptide.  
PN US6218525-B1.  
PD 17-APR-2001.  
PA (GENE) GEN HOSPITAL CORP.  
Query Match 7.5%; Score 133.5; DB 4; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00074;  
RESULT 1406  
ID ADD25530 standard; protein; 351 AA.  
DE Binding domain-immunoglobulin fusion protein-associated protein #42.  
PN US2003118592-A1.  
PD 26-JUN-2003.  
PA (GENE) GENE-CRAFT INC.  
Query Match 7.5%; Score 133.5; DB 7; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00074;  
RESULT 1407  
ID ADF76723 standard; protein; 351 AA.  
DE Novel human secreted and transmembrane protein SeqID 398.  
PN WO2003072035-A2.  
PD 04-SEP-2003.  
PA (GENE) GENE-TECH INC.  
Query Match 7.5%; Score 133.5; DB 7; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00074;  
RESULT 1408  
ID ADO49339 standard; protein; 351 AA.  
DE Human CD2 antigen.  
PN US2004072283-A1.  
PD 15-APR-2004.  
PA (SEED) SEED B.  
PA (ALIE) ALLEN J.  
PA (ARUF) ARUFFO A.  
PA (CAME) CAMERINI D.  
PA (LAUF) LAUFFER L.  
PA (OQUE) OQUENDO C.  
PA (SINN) SIMMONS D.  
PA (STAM) STAMENKOVIC I.  
PA (STEN) STENGELIN S.  
PA (AMIO) AMIOT M.  
Query Match 7.5%; Score 133.5; DB 8; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00074;  
RESULT 1409  
ID ADQ18464 standard; protein; 351 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1283.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 7.5%; Score 133.5; DB 8; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00074;  
RESULT 1410  
ID ADP56034 standard; protein; 351 AA.  
DE Human PRO protein sequence SEQ ID NO:2010.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH) GENE-TECH INC.

Query Match 7.5%; Score 133.5; DB 8; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00074;  
RESULT 1411  
ID AAP81178 standard; protein; 360 AA.  
DE Sequence of human T11 sheep erythrocyte glycoprotein (T11) cDNA deduced from PBI.  
PN EP260880-A.  
PD 23-MAR-1988.  
PA (DAND) DANA FARBER CANCER INST INC.  
Query Match 7.5%; Score 133.5; DB 1; Length 360;  
Best Local Similarity 23.9%; Pred. No. 0.00076;  
RESULT 1412  
ID AAB43688 standard; protein; 737 AA.  
DE Human cancer associated protein sequence SEQ ID NO:1133.  
PN WO200055350-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.5%; Score 133.5; DB 3; Length 737;  
Best Local Similarity 22.3%; Pred. No. 0.0022;  
RESULT 1413  
ID ABU04810 standard; protein; 737 AA.  
DE Human expressed protein tag (EPT) #1476.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 7.5%; Score 133.5; DB 6; Length 737;  
Best Local Similarity 22.3%; Pred. No. 0.0022;  
RESULT 1414  
ID AAR28366 standard; protein; 225 AA.  
DE Sheep LFA-3 protein.  
PN EP517174-A2.  
PD 09-DEC-1992.  
PA (KANF) KANEKAFUCHI KAGAKU KOGYO KK.  
Query Match 7.4%; Score 131; DB 2; Length 225;  
Best Local Similarity 25.0%; Pred. No. 0.00067;  
RESULT 1415  
ID AAR34373 standard; protein; 351 AA.  
DE Sequence encoded by a naturally occurring human CD2.  
PN WO9306866-A2.  
PD 15-APR-1993.  
PA (BIOJ) BIOGEN INC.  
Query Match 7.4%; Score 130.5; DB 2; Length 351;  
Best Local Similarity 23.2%; Pred. No. 0.0014;  
RESULT 1416  
ID AAR54714 standard; protein; 526 AA.  
DE Carcinoembryonic antigen CEA-(c).  
PN US5274087-A.  
PD 28-DEC-1993.  
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.  
Query Match 7.4%; Score 130.5; DB 2; Length 526;  
Best Local Similarity 26.1%; Pred. No. 0.0026;  
RESULT 1417  
ID AAR60314 standard; protein; 225 AA.  
DE Sheep LFA-3.  
PN JP06157334-A.  
PD 03-JUN-1994.  
PA (KANF) KANEBUCHI KAGAKU KOGYO KK.  
Query Match 7.2%; Score 128; DB 2; Length 225;  
Best Local Similarity 24.9%; Pred. No. 0.0013;  
RESULT 1418  
ID AAR06434 standard; protein; 321 AA.  
DE SP1-like protein encoded by clone his1.  
PN WO9007937-A.  
PD 26-JUL-1990.  
PA (OKLA-) OKLAHOMA MED RES FO.  
Query Match 7.2%; Score 128; DB 2; Length 321;  
Best Local Similarity 23.5%; Pred. No. 0.0022;  
RESULT 1419  
ID ABU05236 standard; protein; 321 AA.  
DE Human expressed protein tag (EPT) #1902.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.

Query Match  
Best Local Similarity 7.2%; Score 128; DB 6; Length 321;  
RESULT 1420  
ID AAY43139 standard; protein; 451 AA.  
DE NAIL-Fc protein sequence.  
PN WO9950297-A1.  
PD 07-OCT-1999.  
PA (IMV) IMMUNEX CORP.  
Query Match  
Best Local Similarity 7.2%; Score 128; DB 2; Length 451;  
RESULT 1421  
ID ADE06867 standard; protein; 697 AA.  
DE Novel protein (useful for identifying genetic disorders) #842.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HISE-) HYSEQ INC.  
Query Match  
Best Local Similarity 7.2%; Score 128; DB 7; Length 697;  
RESULT 1422  
ID AAU74427 standard; protein; 240 AA.  
DE Mouse protein sequence #4, related to isolation of genes within SLR-1B.  
PN WO200188200-A2.  
PD 22-NOV-2001.  
PA (ITEX) UNIV TEXAS SYSTEM.  
Query Match  
Best Local Similarity 7.1%; Score 126.5; DB 5; Length 240;  
RESULT 1423  
ID AAY43140 standard; protein; 243 AA.  
DE NAIL-Flag-polyHis protein sequence.  
PN WO9950297-A1.  
PD 07-OCT-1999.  
PA (IMV) IMMUNEX CORP.  
Query Match  
Best Local Similarity 7.1%; Score 126.5; DB 2; Length 243;  
RESULT 1424  
ID AAY43141 standard; protein; 272 AA.  
DE NAIL-L2-polyHis protein sequence.  
PN WO9950297-A1.  
PD 07-OCT-1999.  
PA (IMV) IMMUNEX CORP.  
Query Match  
Best Local Similarity 7.1%; Score 126.5; DB 2; Length 272;  
RESULT 1425  
ID AAB71855 standard; protein; 427 AA.  
DE Human D-SLAM extracellular domain carrying C-terminal HIS tag.  
PN WO200111046-A1.  
PD 15-FEB-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 7.1%; Score 126; DB 4; Length 427;  
RESULT 1426  
ID ABG32414 standard; protein; 427 AA.  
DE D-SLAM protein with C-terminal His tag.  
PN WO200262955-A2.  
PD 15-AUG-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 7.1%; Score 126; DB 5; Length 427;  
RESULT 1427  
ID AAW62480 standard; protein; 856 AA.  
DE Mammalian ZAP-70 protein #1.  
PN JP10313868-A.  
PD 02-DEC-1998.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match  
Best Local Similarity 7.1%; Score 126; DB 2; Length 856;  
RESULT 1428  
ID AAR22045 standard; protein; 321 AA.  
DE Carcino embryonic antigen-related antigen encoded by clone W233.  
PN JP04045788-A.  
PD 14-FEB-1992.  
PA (SUNR) SUNTORY LTD.  
Query Match  
Best Local Similarity 7.1%; Score 125.5; DB 2; Length 321;

Best Local Similarity 25.1%; Pred. No. 0.0039;  
RESULT 1429  
ID ABU04836 standard; protein; 344 AA.  
DE Human expressed protein tag (EPT) #1502.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 7.1%; Score 125.5; DB 6; Length 344;  
RESULT 1430  
ID ABU04804 standard; protein; 344 AA.  
DE Human expressed protein tag (EPT) #1470.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 7.1%; Score 125.5; DB 6; Length 344;  
RESULT 1431  
ID ABU04839 standard; protein; 344 AA.  
DE Human expressed protein tag (EPT) #1505.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 7.1%; Score 125.5; DB 6; Length 344;  
RESULT 1432  
ID AAR22318 standard; protein; 351 AA.  
DE Carcino embryonic antigen-related antigen encoded by clone W239.  
PN JP04045788-A.  
PD 14-FEB-1992.  
PA (SUNR) SUNTORY LTD.  
Query Match  
Best Local Similarity 7.1%; Score 125.5; DB 2; Length 351;  
RESULT 1433  
ID AAP93996 standard; protein; 368 AA.  
DE Transmembrane-4 carcinoembryonic antigen amino acid sequence.  
PN EP346710-A.  
PD 20-DEC-1989.  
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.  
Query Match  
Best Local Similarity 7.1%; Score 125.5; DB 1; Length 368;  
RESULT 1434  
ID AAR22044 standard; protein; 417 AA.  
DE Carcino embryonic antigen-related antigen encoded by clone W211.  
PN JP04045788-A.  
PD 14-FEB-1992.  
PA (SUNR) SUNTORY LTD.  
Query Match  
Best Local Similarity 7.1%; Score 125.5; DB 2; Length 417;  
RESULT 1435  
ID AAP93994 standard; protein; 430 AA.  
DE Sequence of transmembrane (TM)-2 carcinoembryonic antigen (CEA)-(C).  
PN EP346710-A.  
PD 20-DEC-1989.  
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.  
Query Match  
Best Local Similarity 7.1%; Score 125.5; DB 1; Length 430;  
RESULT 1436  
ID AAP93995 standard; protein; 464 AA.  
DE Transmembrane-3 carcinoembryonic antigen amino acid sequence.  
PN EP346710-A.  
PD 20-DEC-1989.  
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.  
Query Match  
Best Local Similarity 7.1%; Score 125.5; DB 1; Length 464;  
RESULT 1437  
ID AAR65166 standard; protein; 464 AA.  
DE Biliary glycoprotein.  
PN WO9506067-A1.  
PD 02-MAR-1995.  
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.  
Query Match  
Best Local Similarity 7.1%; Score 125.5; DB 2; Length 464;

RESULT 1438  
ID AAR77436 standard; protein; 468 AA.  
DE BGP (1-314)/CEA (490-643) chimaeric protein.  
PN WO9506067-A1.  
PD 02-WAR-1995.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
Query Match 7.1%; Score 125.5; DB 2; Length 468;  
Best Local Similarity 25.1%; Pred. No. 0.0067;  
RESULT 1439  
ID AAR77435 standard; protein; 493 AA.  
DE BGP (1-314)/CEA (490-C-terminal) chimaeric protein.  
PN WO9506067-A1.  
PD 02-WAR-1995.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
Query Match 7.1%; Score 125.5; DB 2; Length 493;  
Best Local Similarity 25.1%; Pred. No. 0.0072;  
RESULT 1440  
ID AAR77437 standard; protein; 509 AA.  
DE BGP (1-314)/CEA (490-644)/BGP (391-430) chimaeric protein.  
PN WO9506067-A1.  
PD 02-WAR-1995.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
Query Match 7.1%; Score 125.5; DB 2; Length 509;  
Best Local Similarity 25.1%; Pred. No. 0.0076;  
RESULT 1441  
ID AAR77438 standard; protein; 511 AA.  
DE BGP (1-314)/CEA (490-642)/BGP (387-430) chimaeric protein.  
PN WO9506067-A1.  
PD 02-WAR-1995.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
Query Match 7.1%; Score 125.5; DB 2; Length 511;  
Best Local Similarity 25.1%; Pred. No. 0.0076;  
RESULT 1442  
ID AAP81223 standard; protein; 526 AA.  
DE FL-CEA or carcinoembryonic antigen-C.  
PN EP263933-A.  
PD 20-APR-1988.  
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.  
Query Match 7.1%; Score 125.5; DB 1; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0079;  
RESULT 1443  
ID AAW06873 standard; protein; 526 AA.  
DE Carcinoembryonic antigen CEA-C.  
PN US5571710-A.  
PD 05-NOV-1996.  
PA (FARB ) BAYER CORP.  
Query Match 7.1%; Score 125.5; DB 2; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0079;  
RESULT 1444  
ID AAW83138 standard; protein; 526 AA.  
DE FL-CEA protein.  
PN US5843761-A.  
PD 01-DEC-1998.  
PA (FARB ) BAYER CORP FORMERLY MOLECULAR DIAGNOSTIC.  
Query Match 7.1%; Score 125.5; DB 2; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0079;  
RESULT 1445  
ID ADL15001 standard; protein; 526 AA.  
DE Human carcinoembryonic antigen BGP protein for cancer treatment.  
PN WO2003068268-A2.  
PD 21-AUG-2003.  
PA (BIOI-) BIOINVENT INT AB.  
Query Match 7.1%; Score 125.5; DB 7; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0079;  
RESULT 1446  
ID ADN95238 standard; protein; 526 AA.  
DE Human BEC/LEC-related protein sequence SeqID160.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
Query Match 7.1%; Score 125.5; DB 7; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0079;

RESULT 1447  
ID ADQ17310 standard; protein; 526 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 127.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 7.1%; Score 125.5; DB 8; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0079;  
RESULT 1448  
ID ADQ17232 standard; protein; 526 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 48.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 7.1%; Score 125.5; DB 8; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0079;  
RESULT 1449  
ID ADQ29706 standard; protein; 526 AA.  
DE Human colorectal cancer-associated protein #61.  
PN EP1439393-A2.  
PD 21-JUL-2004.  
PA (FARB ) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 7.1%; Score 125.5; DB 8; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0079;  
RESULT 1450  
ID ADR67261 standard; protein; 526 AA.  
DE Human bladder cancer associated amino acid sequence.  
PN WO2004076613-A2.  
PD 10-SEP-2004.  
PA (HERR/) HERR A.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL B.  
PA (STAU/) STAUB E.  
PA (PILA/) PILARSKY C.  
PA (SPEC/) SPECHT T.  
Query Match 7.1%; Score 125.5; DB 8; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.0079;  
RESULT 1451  
ID ABJ37104 standard; protein; 437 AA.  
DE Concatameric immunoadhesion human protein sequence SEQ ID No 14.  
PN WO2003010202-A1.  
PD 06-FEB-2003.  
PA (MEDE-) MEDEXGEN CO LTD.  
Query Match 7.1%; Score 125; DB 6; Length 437;  
Best Local Similarity 23.5%; Pred. No. 0.0068;  
RESULT 1452  
ID ADQ79912 standard; protein; 437 AA.  
DE Human CD2/Ig construct.  
PN KR2004009997-A.  
PD 31-JAN-2004.  
PA (MEDE-) MEDEXGEN INC.  
Query Match 7.1%; Score 125; DB 8; Length 437;  
Best Local Similarity 23.5%; Pred. No. 0.0068;  
RESULT 1453  
ID ABU37106 standard; protein; 617 AA.  
DE Concatameric immunoadhesion human protein sequence SEQ ID No 18.  
PN WO2003010202-A1.  
PD 06-FEB-2003.  
PA (MEDE-) MEDEXGEN CO LTD.  
Query Match 7.1%; Score 125; DB 6; Length 617;  
Best Local Similarity 23.5%; Pred. No. 0.011;  
RESULT 1454  
ID ABJ37108 standard; protein; 617 AA.  
DE Concatameric immunoadhesion human protein sequence SEQ ID No 22.  
PN WO2003010202-A1.  
PD 06-FEB-2003.  
PA (MEDE-) MEDEXGEN CO LTD.  
Query Match 7.1%; Score 125; DB 6; Length 617;  
Best Local Similarity 23.5%; Pred. No. 0.011;  
RESULT 1455  
ID ADQ79916 standard; protein; 617 AA.  
DE Human CD2-CD2/Ig construct.

PN KR2004009997-A.  
PD 31-JAN-2004.  
PA (MEDE-) MEDEXGEN INC. 7.1%; Score 125; DB 8; Length 617;  
Query Match 23.5%; Pred. No. 0.011;  
Best Local Similarity 23.5%; Pred. No. 0.011;  
RESULT 1456  
ID ADQ79920 standard; protein; 617 AA.  
DE Human mCD2-CD2/Ig construct.  
PN KR2004009997-A.  
PD 31-JAN-2004.  
PA (MEDE-) MEDEXGEN INC. 7.1%; Score 125; DB 8; Length 617;  
Query Match 23.5%; Pred. No. 0.011;  
Best Local Similarity 23.5%; Pred. No. 0.011;  
RESULT 1457  
ID ADF14932 standard; protein; 820 AA.  
DE Human albumin therapeutic fusion protein SeqID228.  
PN WO2003060071-A2.  
PD 24-JUL-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (DELZ) DELTA BIOTECHNOLOGY LTD.  
PA (PRIN-) PRINCIPIA PHARM CORP.  
Query Match 7.1%; Score 125; DB 7; Length 820;  
Best Local Similarity 25.1%; Pred. No. 0.017;  
RESULT 1458  
ID AAP81225 standard; protein; 344 AA.  
DE Carcinoembryonic antigen-D.  
PN EP263933-A.  
PD 20-APR-1988.  
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.  
Query Match 7.0%; Score 124.5; DB 1; Length 344;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1459  
ID AAP94000 standard; protein; 344 AA.  
DE Sequence of CEA antigen pcB720 (CEA-(d)).  
PN EP346710-A.  
PD 20-DEC-1989.  
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.  
Query Match 7.0%; Score 124.5; DB 1; Length 344;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1460  
ID AAR54715 standard; protein; 344 AA.  
DE Carcinoembryonic antigen CEA-(d).  
PN US5274087-A.  
PD 28-DEC-1993.  
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.  
Query Match 7.0%; Score 124.5; DB 2; Length 344;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1461  
ID AAW06874 standard; protein; 344 AA.  
DE Carcinoembryonic antigen CEA-d.  
PN US5571710-A.  
PD 05-NOV-1996.  
PA (FARB) BAYER CORP.  
Query Match 7.0%; Score 124.5; DB 2; Length 344;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1462  
ID ABP68634 standard; protein; 344 AA.  
DE Human pancreatic cancer expressed protein SEQ ID NO 4554.  
PN WO200260317-A2.  
PD 08-AUG-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 7.0%; Score 124.5; DB 5; Length 344;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1463  
ID ABJ37026 standard; protein; 344 AA.  
DE Human breast cancer / ovarian cancer related protein #2.  
PN WO2003000012-A2.  
PD 03-JAN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.0%; Score 124.5; DB 6; Length 344;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1464  
ID ABUS6713 standard; protein; 344 AA.  
DE Respiratory disease differentially expressed protein #57.  
DE Lung cancer-associated polypeptide #306.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC. 7.0%; Score 124.5; DB 6; Length 344;  
Query Match 22.4%; Pred. No. 0.0053;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1465  
ID ABU04820 standard; protein; 344 AA.  
DE Human expressed protein tag (EPT) #1486.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC. 7.0%; Score 124.5; DB 6; Length 344;  
Query Match 22.4%; Pred. No. 0.0053;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1466  
ID ABU04577 standard; protein; 344 AA.  
DE Human expressed protein tag (EPT) #1243.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC. 7.0%; Score 124.5; DB 6; Length 344;  
Query Match 22.4%; Pred. No. 0.0053;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1467  
ID ABU04576 standard; protein; 344 AA.  
DE Human expressed protein tag (EPT) #1242.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC. 7.0%; Score 124.5; DB 6; Length 344;  
Query Match 22.4%; Pred. No. 0.0053;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1468  
ID ABU04826 standard; protein; 344 AA.  
DE Human expressed protein tag (EPT) #1492.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC. 7.0%; Score 124.5; DB 6; Length 344;  
Query Match 22.4%; Pred. No. 0.0053;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1469  
ID ABU04579 standard; protein; 344 AA.  
DE Human expressed protein tag (EPT) #1245.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC. 7.0%; Score 124.5; DB 6; Length 344;  
Query Match 22.4%; Pred. No. 0.0053;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1470  
ID ABU04840 standard; protein; 344 AA.  
DE Human expressed protein tag (EPT) #1506.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC. 7.0%; Score 124.5; DB 6; Length 344;  
Query Match 22.4%; Pred. No. 0.0053;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1471  
ID ABU04797 standard; protein; 344 AA.  
DE Human expressed protein tag (EPT) #1463.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC. 7.0%; Score 124.5; DB 6; Length 344;  
Query Match 22.4%; Pred. No. 0.0053;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1472  
ID ADN39118 standard; protein; 344 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:436.  
PN WO2003042861-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC. 7.0%; Score 124.5; DB 7; Length 344;  
Query Match 22.4%; Pred. No. 0.0053;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1473  
ID ADK70491 standard; protein; 344 AA.  
DE Respiratory disease differentially expressed protein #57.

PN WO2003101283-A2.  
PD 11-DEC-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 7.0%; Score 124.5; DB 8; Length 344;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1474  
ID ADO49155 standard; peptide; 344 AA.  
DE Human nonspecific crossreacting antigen protein.  
PN WO2004031238-A2.  
PD 15-APR-2004.  
PA (UYWC-) UNIV MCGILL.  
Query Match 7.0%; Score 124.5; DB 8; Length 344;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1475  
ID ADO28647 standard; protein; 344 AA.  
DE Human NCA protein SEQ ID NO:76.  
PN WO2004044178-A2.  
PD 27-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 7.0%; Score 124.5; DB 8; Length 344;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1476  
ID ADO29709 standard; protein; 344 AA.  
DE Human colorectal cancer-associated protein #64.  
PN EP1439393-A2.  
PD 21-JUL-2004.  
PA (FARB-) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 7.0%; Score 124.5; DB 8; Length 344;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1477  
ID ADO80359 standard; protein; 344 AA.  
DE CEA-related cell adhesion molecule 6 protein.  
PN WO2004063709-A2.  
PD 29-JUL-2004.  
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.  
Query Match 7.0%; Score 124.5; DB 8; Length 344;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1478  
ID ADR67262 standard; protein; 344 AA.  
DE Human bladder cancer associated amino acid sequence.  
PN WO2004076613-A2.  
PD 10-SEP-2004.  
PA (HERR-) HERR A.  
PA (HINZ-) HINZMANN B.  
PA (DAHL-) DAHL E.  
PA (STAU-) STAUB E.  
PA (PILA-) PILARSKY C.  
PA (SPEC-) SPECHT T.  
Query Match 7.0%; Score 124.5; DB 8; Length 344;  
Best Local Similarity 22.4%; Pred. No. 0.0053;  
RESULT 1479  
ID AAM24171 standard; protein; 159 AA.  
DE Murine EST encoded protein SEQ ID NO: 1696.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.0%; Score 123.5; DB 4; Length 159;  
Best Local Similarity 35.0%; Pred. No. 0.0022;  
RESULT 1480  
ID AAG75121 standard; protein; 365 AA.  
DE Human colon cancer antigen protein SEQ ID NO:5885.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.0%; Score 123.5; DB 4; Length 365;  
Best Local Similarity 22.4%; Pred. No. 0.0073;  
RESULT 1481  
ID ABU04814 standard; protein; 365 AA.  
DE Human expressed protein tag (BPT) #1480.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.9%; Score 122; DB 7; Length 211;  
Best Local Similarity 29.8%; Pred. No. 0.0046;  
RESULT 1482  
ID AAR28367 standard; protein; 199 AA.  
DE LFA-3 TM region deficient protein.  
PN EP517174-A2.  
PD 09-DEC-1992.  
PA (KANF-) KANEGAFUCHI KAGAKU KOGYO KK.  
Query Match 6.9%; Score 123; DB 2; Length 199;  
Best Local Similarity 25.4%; Pred. No. 0.0033;  
RESULT 1483  
ID AAR60311 standard; protein; 199 AA.  
DE Sheep LFA-3 delta TM protein.  
PN JP06157334-A.  
PD 03-JUN-1994.  
PA (KANF-) KANEBUCHI KAGAKU KOGYO KK.  
Query Match 6.9%; Score 123; DB 2; Length 199;  
Best Local Similarity 25.4%; Pred. No. 0.0033;  
RESULT 1484  
ID AAB71856 standard; protein; 223 AA.  
DE Human D-SIAM extracellular domain carrying N-terminal His-tag.  
PN WO200111046-A1.  
PD 15-FEB-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.9%; Score 123; DB 4; Length 223;  
Best Local Similarity 25.9%; Pred. No. 0.004;  
RESULT 1485  
ID ABG32415 standard; protein; 223 AA.  
DE D-SIAM protein with N-terminal His tag.  
PN WO200262955-A2.  
PD 15-AUG-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.9%; Score 123; DB 5; Length 223;  
Best Local Similarity 25.9%; Pred. No. 0.004;  
RESULT 1486  
ID AAW83139 standard; protein; 344 AA.  
DE BT20 protein.  
PN US5843761-A.  
PD 01-DEC-1998.  
PA (FARB-) BAYER CORP FORMERLY MOLECULAR DIAGNOSTIC.  
Query Match 6.9%; Score 122.5; DB 2; Length 344;  
Best Local Similarity 22.4%; Pred. No. 0.0083;  
RESULT 1487  
ID ABU04831 standard; protein; 344 AA.  
DE Human expressed protein tag (BPT) #1497.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.9%; Score 122.5; DB 6; Length 344;  
Best Local Similarity 22.4%; Pred. No. 0.0083;  
RESULT 1488  
ID ABW01439 standard; protein; 211 AA.  
DE Human TANGO 195 form 2 protein extracellular domain.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 6.9%; Score 122; DB 7; Length 211;  
Best Local Similarity 29.8%; Pred. No. 0.0046;  
RESULT 1489  
ID ABW01420 standard; protein; 211 AA.  
DE Human TANGO 195 form 1 protein extracellular domain.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 6.9%; Score 122; DB 7; Length 211;  
Best Local Similarity 29.8%; Pred. No. 0.0046;  
RESULT 1490  
ID ABW01445 standard; protein; 211 AA.  
DE Human TANGO 195 protein extracellular domain.  
PN US2003113865-A1.  
PD 19-JUN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 6.9%; Score 122; DB 7; Length 211;



Best Local Similarity 29.8%; Pred. No. 0.0046;  
RESULT 1491  
ID ABG75380 standard; protein; 246 AA.  
DE INSP052 extracellular domain protein.  
PN WO2003093316-A2.  
PD 13-NOV-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 6.9%; Score 122; DB 7; Length 246;  
Best Local Similarity 25.4%; Pred. No. 0.0057;  
RESULT 1492  
ID ADO47887 standard; protein; 270 AA.  
DE Human protein SEQ ID NO:4.  
PN WO2004007672-A2.  
PD 22-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 6.9%; Score 122; DB 8; Length 270;  
Best Local Similarity 25.4%; Pred. No. 0.0065;  
RESULT 1493  
ID ADS11055 standard; protein; 270 AA.  
DE Human therapeutic protein - SEQ ID 1292.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 6.9%; Score 122; DB 8; Length 270;  
Best Local Similarity 25.4%; Pred. No. 0.0065;  
RESULT 1494  
ID AAE14784 standard; protein; 298 AA.  
DE Human immunoglobulin superfamily protein (IGSFP)-4.  
PN WO200240671-A2.  
PD 23-MAY-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 6.9%; Score 122; DB 5; Length 298;  
Best Local Similarity 25.4%; Pred. No. 0.0076;  
RESULT 1495  
ID ADK40854 standard; protein; 316 AA.  
DE Human A33 molecule.  
PN US669688-B1.  
PD 02-MAR-2004.  
PA (UINY) UNIV NEW YORK STATE RES FOUND.  
Query Match 6.9%; Score 122; DB 8; Length 316;  
Best Local Similarity 23.0%; Pred. No. 0.0082;  
RESULT 1496  
ID AAP90046 standard; protein; 344 AA.  
DE Human nonspecific cross-reacting antigen protein.  
PN JP01120289-A.  
PD 12-MAY-1989.  
PA (SUNR) SUNTORY LTD.  
Query Match 6.9%; Score 121.5; DB 1; Length 344;  
Best Local Similarity 22.1%; Pred. No. 0.01;  
RESULT 1497  
ID ABU04578 standard; protein; 344 AA.  
DE Human expressed protein tag (EPT) #1244.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.9%; Score 121.5; DB 6; Length 344;  
Best Local Similarity 22.1%; Pred. No. 0.01;  
RESULT 1498  
ID AAR60316 standard; protein; 199 AA.  
DE Sheep LFA-3 delta TM.  
PN JP06157334-A.  
PD 03-JUN-1994.  
PA (KANF) KANEBUCHI KAGAKU KOGYO KK.  
Query Match 6.8%; Score 121; DB 2; Length 199;  
Best Local Similarity 25.5%; Pred. No. 0.0052;  
RESULT 1499  
ID AAY72878 standard; protein; 352 AA.  
DE Human PROS723 protein encoded by DNA82361 cDNA clone.  
PN WO200116319-A2.  
PD 08-MAR-2001.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 120; DB 4; Length 352;  
Best Local Similarity 22.3%; Pred. No. 0.015;  
RESULT 1500  
ID AAB50930 standard; protein; 352 AA.  
DE Human PROS723 protein.  
PN WO200073452-A2.  
PD 07-DEC-2000.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 120; DB 4; Length 352;  
Best Local Similarity 22.3%; Pred. No. 0.015;

**This Page Blank (uspto)**

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 14, 2005, 13:23:03 ; Search time 22 Seconds  
(without alignments)  
1136.702 Million cell updates/sec

Title: US-10-063-551-46

Perfect score: 1772

Sequence: 1 MAGSPCTLIVILWQLTGS.....PHSLITMDPTRLPAYENVI 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	28.1	97	4	US-09-513-999C-4472
2	362.5	20.5	328	4	US-09-949-016-6428
3	362.5	20.5	329	4	US-09-149-476-483
4	362.5	20.5	332	4	US-09-949-016-7327
5	186	10.5	343	1	US-08-348-792-10
6	186	10.5	343	3	US-08-462-738-10
7	186	10.5	343	3	US-09-199-955-10
8	186	10.5	343	3	US-08-880-875-10
9	182.5	10.3	335	1	US-08-348-792-2
10	182.5	10.3	335	2	US-08-462-738-2
11	182.5	10.3	335	3	US-09-199-955-2
12	182.5	10.3	335	3	US-08-880-875-2
13	182.5	10.3	335	4	US-09-369-248A-3
14	180	10.2	307	1	US-08-348-792-8
15	180	10.2	307	2	US-08-462-738-8
16	180	10.2	307	3	US-09-199-955-8
17	180	10.2	307	3	US-08-880-875-8
18	170	9.6	365	4	US-09-949-016-6907
19	170	9.6	391	4	US-09-949-016-7325
20	164.5	9.3	305	1	US-08-348-792-6
21	164.5	9.3	305	2	US-08-462-738-6
22	164.5	9.3	305	3	US-09-199-955-6
23	164.5	9.3	305	3	US-08-880-875-6
24	158.5	8.9	329	1	US-08-348-792-12
25	158.5	8.9	329	2	US-08-462-738-12
26	158.5	8.9	329	3	US-09-199-955-12
27	158.5	8.9	329	3	US-08-880-875-12

28	152	8.6	298	1	US-08-348-792-4	Sequence 4, Appli
29	152	8.6	298	2	US-08-462-738-4	Sequence 4, Appli
30	152	8.6	298	3	US-09-199-955-4	Sequence 4, Appli
31	152	8.6	298	4	US-08-880-875-4	Sequence 4, Appli
32	150.5	8.5	285	4	US-09-369-248A-2	Sequence 2, Appli
33	141	8.0	143	3	US-09-227-357-443	Sequence 443, App
34	140.5	7.9	143	3	US-09-227-357-192	Sequence 192, App
35	136.5	7.7	351	3	US-08-466-465-6	Sequence 6, Appli
36	136.5	7.7	351	4	US-09-730-465-6	Sequence 6, Appli
37	128	7.2	225	1	US-08-328-152A-31	Sequence 31, Appli
38	128	7.2	321	6	5169835-17	Patent No. 5169835
39	128	7.2	321	6	5169835-17	Patent No. 5169835
40	125.5	7.1	464	4	US-08-602-725-32	Sequence 32, Appl
41	125.5	7.1	464	4	US-09-949-016-6116	Sequence 6116, Ap
42	125.5	7.1	464	4	US-09-949-016-7525	Sequence 7525, Ap
43	124.5	7.0	365	4	US-09-949-016-7591	Sequence 7591, Ap
44	123	6.9	199	1	US-08-328-152A-36	Sequence 36, Appli
45	122	6.9	316	4	US-09-397-243D-13	Sequence 13, Appli
46	119.5	6.7	365	2	US-08-979-424-3	Sequence 3, Appli
47	119.5	6.7	365	3	US-09-272-496-2	Sequence 2, Appli
48	119.5	6.7	365	4	US-09-949-016-6064	Sequence 6064, Ap
49	119.5	6.7	383	4	US-09-949-016-11050	Sequence 11050, A
50	119.5	6.7	418	3	US-08-630-172-18	Sequence 18, Appli
51	119.5	6.7	418	3	US-09-375-419-18	Sequence 18, Appli
52	117.5	6.6	344	2	US-08-602-725-34	Sequence 34, Appli
53	117.5	6.6	365	3	US-08-928-383B-2	Sequence 2, Appli
54	116.5	6.6	319	1	US-08-597-495B-22	Sequence 22, Appli
55	116.5	6.6	319	3	US-09-068-051A-22	Sequence 22, Appli
56	116.5	6.6	319	4	US-09-336-536-67	Sequence 67, Appli
57	116.5	6.6	319	4	US-09-254-465A-6	Sequence 6, Appli
58	116.5	6.6	319	4	US-09-953-499-6	Sequence 6, Appli
59	115.5	6.5	184	3	US-08-630-172-2	Sequence 2, Appli
60	115.5	6.5	184	3	US-09-375-419-2	Sequence 2, Appli
61	114.5	6.5	642	1	US-08-217-299-1	Sequence 1, Appli
62	114.5	6.5	698	2	US-08-602-725-36	Sequence 36, Appli
63	114.5	6.5	702	4	US-09-949-016-6484	Sequence 6484, Ap
64	114.5	6.5	734	2	US-08-389-459A-17	Sequence 17, Appli
65	114.5	6.5	734	3	US-08-987-867A-17	Sequence 17, Appli
66	114.5	6.5	740	4	US-09-949-016-8168	Sequence 8168, Ap
67	111.5	6.3	174	2	US-08-765-536-2	Sequence 2, Appli
68	111.5	6.3	174	5	PCT-US95-08401-2	Sequence 2, Appli
69	110.5	6.2	365	4	US-09-899-634C-4	Sequence 4, Appli
70	109.5	6.2	315	4	US-09-910-174B-28	Sequence 28, Appli
71	109.5	6.2	315	4	US-09-620-461-28	Sequence 28, Appli
72	109	6.2	324	4	US-09-910-174B-6	Sequence 6, Appli
73	109	6.2	324	4	US-09-620-461-6	Sequence 6, Appli
74	105.5	6.0	323	4	US-09-651-200-21	Sequence 21, Appli
75	105.5	6.0	323	4	US-09-441-411-22	Sequence 22, Appli
76	105.5	6.0	323	5	PCT-US94-09642-2	Sequence 2, Appli
77	105.5	6.0	329	2	US-08-456-104-2	Sequence 2, Appli
78	105.5	6.0	329	2	US-08-101-624-2	Sequence 2, Appli
79	105.5	6.0	329	3	US-08-479-744A-2	Sequence 2, Appli
80	105.5	6.0	329	3	US-08-280-757B-2	Sequence 2, Appli
81	105.5	6.0	329	3	US-08-205-697A-23	Sequence 23, Appli
82	105.5	6.0	329	3	US-08-702-525-23	Sequence 23, Appli
83	105.5	6.0	329	3	US-08-403-253A-4	Sequence 4, Appli
84	105.5	6.0	329	4	US-08-435-816A-4	Sequence 4, Appli
85	105.5	6.0	329	4	US-09-425-762-2	Sequence 2, Appli
86	105.5	6.0	329	4	US-09-837-867A-23	Sequence 23, Appli
87	105.5	6.0	329	4	US-09-206-132-2	Sequence 2, Appli
88	105.5	6.0	329	4	US-09-441-411-26	Sequence 26, Appli
89	105.5	6.0	329	4	US-09-425-516-2	Sequence 2, Appli
90	105.5	6.0	329	5	PCT-US95-02576-23	Sequence 23, Appli
91	105.5	6.0	372	4	US-09-949-016-11132	Sequence 11132, A
92	104.5	5.9	329	4	US-09-667-135-32	Sequence 32, Appli
93	104	5.9	349	4	US-09-924-103-4	Sequence 4, Appli
94	102	5.8	144	4	US-09-513-999C-4353	Sequence 4353, Ap
95	101.5	5.7	270	4	US-09-254-465A-24	Sequence 24, Appli
96	101.5	5.7	270	4	US-09-953-499-24	Sequence 24, Appli
97	101.5	5.7	273	4	US-09-254-465A-26	Sequence 26, Appli
98	101.5	5.7	273	4	US-09-953-499-26	Sequence 26, Appli
99	100.5	5.7	638	3	US-09-228-986-74	Sequence 74, Appli
100	100.5	5.7	638	4	US-10-101-464A-74	Sequence 74, Appli

101	100	5.6	365	3	US-08-928-383B-24	Sequence 24, Appl	174	90	5.1	253	4	US-09-949-016-10124	Sequence 10124, A
102	98.5	5.6	365	3	US-08-928-383B-23	Sequence 23, Appl	175	90	5.1	419	6	5169835-2	Patent No. 5169835
103	98	5.5	503	4	US-08-999-689A-6	Sequence 6, Appl	176	90	5.1	419	6	5169835-2	Patent No. 5169835
104	98	5.5	503	4	US-09-944-807-4	Sequence 4, Appl	177	90	5.1	541	1	US-08-604-333-2	Sequence 2, Appl
105	97	5.5	773	3	US-08-434-000A-2	Sequence 2, Appl	178	90	5.1	541	1	US-08-110-618-2	Sequence 2, Appl
106	97	5.5	773	3	US-09-312-157-2	Sequence 2, Appl	179	90	5.1	541	3	US-09-173-151A-28	Sequence 28, Appl
107	97	5.5	773	4	US-09-717-888-2	Sequence 2, Appl	180	90	5.1	541	4	US-09-578-178-2	Sequence 2, Appl
108	96.5	5.4	534	4	US-09-651-200-6	Sequence 6, Appl	181	90	5.1	541	4	US-09-577-806-2	Sequence 2, Appl
109	96.5	5.4	534	4	US-09-651-200-24	Sequence 24, Appl	182	90	5.1	541	4	US-09-621-502-4	Sequence 4, Appl
110	96	5.4	340	4	US-09-651-200-2	Sequence 2, Appl	183	89.5	5.1	256	4	US-09-949-016-7326	Sequence 7326, Ap
111	96	5.4	441	4	US-09-651-200-4	Sequence 4, Appl	184	89.5	5.1	423	4	US-09-181-339-9	Sequence 9, Appl
112	96	5.4	526	4	US-09-910-174B-9	Sequence 9, Appl	185	89	5.0	303	4	US-09-651-200-23	Sequence 23, Appl
113	96	5.4	526	4	US-09-620-461-9	Sequence 9, Appl	186	89	5.0	303	4	US-09-441-411-15	Sequence 15, Appl
114	96	5.4	526	4	US-09-949-016-6122	Sequence 6122, Ap	187	89	5.0	303	4	US-09-441-411-20	Sequence 20, Appl
115	96	5.4	540	4	US-09-949-016-11644	Sequence 11644, A	188	89	5.0	309	2	US-08-456-104-4	Sequence 4, Appl
116	95.5	5.4	365	3	US-08-928-383B-26	Sequence 26, Appl	189	89	5.0	309	3	US-08-479-744A-23	Sequence 23, Appl
117	95.5	5.4	417	4	US-09-949-016-6729	Sequence 6729, Ap	190	89	5.0	309	3	US-08-280-757B-23	Sequence 23, Appl
118	95.5	5.4	771	3	US-08-434-000A-8	Sequence 8, Appl	191	89	5.0	309	3	US-08-205-697A-21	Sequence 21, Appl
119	95.5	5.4	771	3	US-09-312-157-8	Sequence 8, Appl	192	89	5.0	309	3	US-08-702-525-21	Sequence 21, Appl
120	95.5	5.4	771	4	US-09-717-888-8	Sequence 8, Appl	193	89	5.0	309	4	US-09-651-200-22	Sequence 22, Appl
121	93.5	5.3	299	3	US-09-188-930-189	Sequence 189, App	194	89	5.0	309	4	US-09-667-135-33	Sequence 33, Appl
122	93.5	5.3	2409	6	5180808-2	Patent No. 5180808	195	89	5.0	309	4	US-09-425-762-23	Sequence 23, Appl
123	93.5	5.3	2409	6	5180808-2	Patent No. 5180808	196	89	5.0	309	4	US-09-837-867A-21	Sequence 21, Appl
124	93	5.2	316	4	US-09-910-174B-24	Sequence 24, Appl	197	89	5.0	309	4	US-09-206-132-4	Sequence 4, Appl
125	93	5.2	316	4	US-09-620-461-24	Sequence 24, Appl	198	89	5.0	309	4	US-09-441-411-13	Sequence 13, Appl
126	93	5.2	561	3	US-09-192-545-2	Sequence 2, Appl	199	89	5.0	309	4	US-09-441-411-18	Sequence 18, Appl
127	92.5	5.2	299	3	US-09-188-930-331	Sequence 331, App	200	89	5.0	309	4	US-09-441-411-24	Sequence 24, Appl
128	92.5	5.2	299	3	US-09-462-270-2	Sequence 2, Appl	201	89	5.0	309	4	US-09-425-516-23	Sequence 23, Appl
129	92.5	5.2	299	4	US-09-254-465A-1	Sequence 1, Appl	202	89	5.0	309	5	PCT-US95-02576-21	Sequence 21, Appl
130	92.5	5.2	299	4	US-09-312-283C-189	Sequence 189, App	203	89	5.0	309	3	US-08-205-697A-13	Sequence 13, Appl
131	92.5	5.2	299	4	US-09-312-283C-331	Sequence 331, App	204	89	5.0	314	3	US-08-702-525-21	Sequence 13, Appl
132	92.5	5.2	299	4	US-09-907-794A-119	Sequence 119, App	205	89	5.0	314	3	US-09-837-867A-13	Sequence 13, Appl
133	92.5	5.2	299	4	US-09-905-125A-119	Sequence 119, App	206	89	5.0	314	4	US-09-441-411-14	Sequence 14, Appl
134	92.5	5.2	299	4	US-09-902-775A-119	Sequence 119, App	207	89	5.0	314	4	US-09-441-411-19	Sequence 19, Appl
135	92.5	5.2	299	4	US-09-397-243D-3	Sequence 3, Appl	208	89	5.0	314	5	PCT-US95-02576-13	Sequence 13, Appl
136	92.5	5.2	299	4	US-09-906-700-119	Sequence 119, App	209	89	5.0	356	4	US-09-441-411-11	Sequence 11, Appl
137	92.5	5.2	299	4	US-09-903-603A-119	Sequence 119, App	210	89	5.0	356	4	US-09-441-411-12	Sequence 12, Appl
138	92.5	5.2	299	4	US-09-904-920A-119	Sequence 119, App	211	89	5.0	356	4	US-09-441-411-16	Sequence 16, Appl
139	92.5	5.2	299	4	US-09-909-064-119	Sequence 119, App	212	89	5.0	356	4	US-09-441-411-17	Sequence 17, Appl
140	92.5	5.2	299	4	US-09-905-381A-119	Sequence 119, App	213	89	5.0	821	3	US-09-422-869-24	Sequence 24, Appl
141	92.5	5.2	299	4	US-09-906-638-119	Sequence 119, App	214	89	5.0	821	4	US-09-538-092-972	Sequence 972, App
142	92.5	5.2	299	4	US-09-953-499-1	Sequence 1, Appl	215	88.5	5.0	237	4	US-08-756-416-36	Sequence 36, Appl
143	92	5.2	491	4	US-09-181-339-12	Sequence 12, Appl	216	88.5	5.0	611	2	US-08-752-307B-10	Sequence 10, Appl
144	91.5	5.2	230	4	US-09-869-388-4	Sequence 4, Appl	217	88.5	5.0	611	3	US-09-991-326-10	Sequence 10, Appl
145	91	5.1	251	6	5185441-38	Patent No. 5185441	218	88.5	5.0	611	3	US-09-651-200-19	Sequence 19, Appl
146	91	5.1	251	6	5185441-38	Patent No. 5185441	219	88	5.0	329	4	US-09-651-200-19	Sequence 19, Appl
147	90.5	5.1	521	3	US-08-996-338-20	Sequence 20, Appl	220	88	5.0	699	1	US-08-348-006B-7	Sequence 7, Appl
148	90.5	5.1	521	4	US-09-556-972-20	Sequence 20, Appl	221	88	5.0	699	2	US-08-800-825A-7	Sequence 7, Appl
149	90	5.1	156	4	US-09-370-838-210	Sequence 210, App	222	88	5.0	699	3	US-09-158-657-7	Sequence 7, Appl
150	90	5.1	156	4	US-09-854-133-210	Sequence 210, App	223	88	5.0	1023	4	US-09-270-767-43827	Sequence 43827, A
151	90	5.1	222	1	US-08-328-152A-8	Sequence 8, Appl	224	87.5	4.9	302	4	US-09-789-697A-21	Sequence 21, Appl
152	90	5.1	240	1	US-07-940-861-12	Sequence 12, Appl	225	87.5	4.9	325	4	US-09-651-200-20	Sequence 20, Appl
153	90	5.1	240	1	US-08-459-532-12	Sequence 12, Appl	226	87.5	4.9	769	3	US-08-434-000A-10	Sequence 10, Appl
154	90	5.1	240	2	US-08-459-657-12	Sequence 12, Appl	227	87.5	4.9	769	3	US-09-342-157-10	Sequence 10, Appl
155	90	5.1	240	2	US-08-460-132-12	Sequence 12, Appl	228	87.5	4.9	769	4	US-09-717-888-10	Sequence 10, Appl
156	90	5.1	240	3	US-08-466-465-4	Sequence 4, Appl	229	87	4.9	490	3	US-09-336-643A-6	Sequence 6, Appl
157	90	5.1	240	4	US-09-730-465-4	Sequence 4, Appl	230	87	4.9	491	4	US-09-181-339-7	Sequence 7, Appl
158	90	5.1	240	5	PCT-US92-02050-12	Sequence 12, Appl	231	87	4.9	507	4	US-09-949-016-9860	Sequence 9860, Ap
159	90	5.1	240	6	5185441-36	Patent No. 5185441	232	87	4.9	582	4	US-09-702-705-334	Sequence 334, App
160	90	5.1	240	6	5223394-4	Patent No. 5223394	233	87	4.9	582	4	US-09-736-457-334	Sequence 334, App
161	90	5.1	240	6	5223394-6	Patent No. 5223394	234	87	4.9	582	4	US-09-614-124B-334	Sequence 334, App
162	90	5.1	240	6	5185441-36	Patent No. 5185441	235	87	4.9	582	4	US-09-671-325-334	Sequence 334, App
163	90	5.1	240	6	5223394-4	Patent No. 5223394	236	87	4.9	582	4	US-09-589-184-334	Sequence 334, App
164	90	5.1	240	6	5223394-6	Patent No. 5223394	237	87	4.9	582	4	US-09-658-824-334	Sequence 334, App
165	90	5.1	250	1	US-07-940-861-10	Sequence 10, Appl	238	87	4.9	583	2	US-08-432-016-2	Sequence 2, Appl
166	90	5.1	250	1	US-08-459-512-10	Sequence 10, Appl	239	87	4.9	583	2	US-08-684-594-2	Sequence 2, Appl
167	90	5.1	250	2	US-08-459-657-10	Sequence 10, Appl	240	86.5	4.9	790	3	US-08-960-780-4	Sequence 4, Appl
168	90	5.1	250	2	US-08-460-132-10	Sequence 10, Appl	241	86.5	4.9	790	3	US-09-073-898-4	Sequence 4, Appl
169	90	5.1	250	3	US-08-466-465-2	Sequence 2, Appl	242	86.5	4.9	790	4	US-09-850-351A-4	Sequence 4, Appl
170	90	5.1	250	4	US-08-730-465-2	Sequence 2, Appl	243	86	4.9	302	4	US-09-877-730-14	Sequence 14, Appl
171	90	5.1	250	5	PCT-US92-02050-10	Sequence 10, Appl	244	86	4.9	380	4	US-09-877-730-4	Sequence 4, Appl
172	90	5.1	250	5	5223394-1	Patent No. 5223394	245	86	4.9	604	4	US-09-949-016-9548	Sequence 9548, Ap
173	90	5.1	250	6	5223394-1	Patent No. 5223394	246	86	4.9	826	4	US-09-877-730-16	Sequence 16, Appl

247	86	4.9	904	4	US-09-877-730-6	Sequence 6, Appl	320	83.5	4.7	263	4	US-09-953-499-25	Sequence 25, Appl
248	86	4.9	907	4	US-09-877-730-20	Sequence 20, Appl	321	83.5	4.7	298	4	US-09-152-060-76	Sequence 76, Appl
249	86	4.9	985	4	US-09-877-730-10	Sequence 10, Appl	322	83.5	4.7	312	4	US-09-254-465A-9	Sequence 9, Appl
250	86	4.9	991	4	US-09-877-730-12	Sequence 12, Appl	323	83.5	4.7	312	4	US-09-907-794A-64	Sequence 64, Appl
251	86	4.9	1069	4	US-09-877-730-2	Sequence 2, Appl	324	83.5	4.7	312	4	US-09-905-125A-64	Sequence 64, Appl
252	86	4.9	1072	4	US-09-877-730-18	Sequence 18, Appl	325	83.5	4.7	312	4	US-09-902-775A-64	Sequence 64, Appl
253	86	4.9	1150	4	US-09-877-730-8	Sequence 8, Appl	326	83.5	4.7	312	4	US-09-906-700-64	Sequence 64, Appl
254	85.5	4.8	746	2	US-08-838-2198-6	Sequence 6, Appl	327	83.5	4.7	312	4	US-09-903-603A-64	Sequence 64, Appl
255	85.5	4.8	746	3	US-09-233-336A-6	Sequence 6, Appl	328	83.5	4.7	312	4	US-09-904-920A-64	Sequence 64, Appl
256	85.5	4.8	746	3	US-09-233-752A-6	Sequence 6, Appl	329	83.5	4.7	312	4	US-09-909-064-64	Sequence 64, Appl
257	85.5	4.8	746	3	US-09-402-036-6	Sequence 6, Appl	330	83.5	4.7	312	4	US-09-905-381A-64	Sequence 64, Appl
258	85.5	4.8	746	4	US-09-904-226-6	Sequence 6, Appl	331	83.5	4.7	312	4	US-09-906-618A-64	Sequence 64, Appl
259	85.5	4.8	789	1	US-08-471-033-29	Sequence 29, Appl	332	83.5	4.7	312	4	US-09-953-499-9	Sequence 9, Appl
260	85.5	4.8	789	1	US-08-471-033-32	Sequence 32, Appl	333	83.5	4.7	318	3	US-09-068-051A-32	Sequence 32, Appl
261	85.5	4.8	789	2	US-08-471-044-29	Sequence 29, Appl	334	83.5	4.7	391	4	US-08-999-689A-8	Sequence 8, Appl
262	85.5	4.8	789	2	US-08-471-044-32	Sequence 32, Appl	335	83.5	4.7	408	3	US-09-724-864-62	Sequence 62, Appl
263	85.5	4.8	789	2	US-08-463-483A-29	Sequence 29, Appl	336	83.5	4.7	450	4	US-09-907-794A-320	Sequence 320, Appl
264	85.5	4.8	789	2	US-08-463-483A-32	Sequence 32, Appl	337	83.5	4.7	450	4	US-09-905-125A-320	Sequence 320, Appl
265	85.5	4.8	789	2	US-08-471-046A-29	Sequence 29, Appl	338	83.5	4.7	450	4	US-09-902-775A-320	Sequence 320, Appl
266	85.5	4.8	789	2	US-08-471-046A-32	Sequence 32, Appl	339	83.5	4.7	450	4	US-09-906-700-320	Sequence 320, Appl
267	85.5	4.8	789	2	US-08-470-566B-29	Sequence 29, Appl	340	83.5	4.7	450	4	US-09-903-603A-320	Sequence 320, Appl
268	85.5	4.8	789	2	US-08-470-566B-32	Sequence 32, Appl	341	83.5	4.7	450	4	US-09-904-920A-320	Sequence 320, Appl
269	85.5	4.8	789	2	US-08-838-2198-2	Sequence 2, Appl	342	83.5	4.7	450	4	US-09-909-064-320	Sequence 320, Appl
270	85.5	4.8	789	2	US-08-838-2198-4	Sequence 4, Appl	343	83.5	4.7	450	4	US-09-905-381A-320	Sequence 320, Appl
271	85.5	4.8	789	2	US-08-469-334-29	Sequence 29, Appl	344	83.5	4.7	450	4	US-09-906-618-320	Sequence 320, Appl
272	85.5	4.8	789	2	US-08-469-334-32	Sequence 32, Appl	345	83.5	4.7	789	3	US-09-002-285-96	Sequence 96, Appl
273	85.5	4.8	789	3	US-09-300-529-29	Sequence 29, Appl	346	83.5	4.7	789	4	US-09-589-477-96	Sequence 96, Appl
274	85.5	4.8	789	3	US-09-300-529-32	Sequence 32, Appl	347	83.5	4.7	789	4	US-10-099-285A-96	Sequence 96, Appl
275	85.5	4.8	789	3	US-09-300-529-32	Sequence 32, Appl	348	83.5	4.7	1501	2	US-08-447-464-3	Sequence 3, Appl
276	85.5	4.8	789	3	US-09-233-336A-4	Sequence 4, Appl	349	83.5	4.7	1501	2	US-08-716-679-3	Sequence 3, Appl
277	85.5	4.8	789	3	US-09-233-336A-2	Sequence 2, Appl	350	83	4.7	464	4	US-09-297-468-2	Sequence 2, Appl
278	85.5	4.8	789	3	US-09-233-752A-2	Sequence 2, Appl	351	83	4.7	846	1	US-08-149-103-3	Sequence 3, Appl
279	85.5	4.8	789	3	US-09-402-036-2	Sequence 2, Appl	352	83	4.7	846	1	US-08-451-883-3	Sequence 3, Appl
280	85.5	4.8	789	3	US-09-402-036-4	Sequence 4, Appl	353	83	4.7	873	1	US-08-393-734-2	Sequence 2, Appl
281	85.5	4.8	789	3	US-09-002-285-78	Sequence 78, Appl	354	83	4.7	873	3	US-08-894-489-2	Sequence 2, Appl
282	85.5	4.8	789	3	US-09-002-285-80	Sequence 80, Appl	355	83	4.7	894	4	US-09-949-016-10605	Sequence 10605, A
283	85.5	4.8	789	3	US-09-002-285-94	Sequence 94, Appl	356	83	4.7	904	4	US-09-949-016-9528	Sequence 9528, Ap
284	85.5	4.8	789	3	US-09-002-285-100	Sequence 100, Appl	357	82.5	4.7	194	3	US-08-630-172-14	Sequence 14, Appl
285	85.5	4.8	789	4	US-09-904-226-2	Sequence 2, Appl	358	82.5	4.7	194	3	US-09-375-419-14	Sequence 14, Appl
286	85.5	4.8	789	4	US-09-904-226-4	Sequence 4, Appl	359	82.5	4.7	226	4	US-09-869-388-10	Sequence 10, Appl
287	85.5	4.8	789	4	US-09-589-477-78	Sequence 78, Appl	360	82.5	4.7	238	4	US-09-149-476-485	Sequence 485, App
288	85.5	4.8	789	4	US-09-589-477-80	Sequence 80, Appl	361	82.5	4.7	456	4	US-09-949-016-7564	Sequence 7564, Ap
289	85.5	4.8	789	4	US-09-589-477-94	Sequence 94, Appl	362	82.5	4.7	486	4	US-09-134-000C-5552	Sequence 5552, Ap
290	85.5	4.8	789	4	US-09-589-477-100	Sequence 100, Appl	363	82.5	4.7	511	3	US-09-002-285-88	Sequence 88, Appl
291	85.5	4.8	789	4	US-10-099-285A-78	Sequence 78, Appl	364	82.5	4.7	511	4	US-09-589-477-88	Sequence 88, Appl
292	85.5	4.8	789	4	US-10-099-285A-80	Sequence 80, Appl	365	82.5	4.7	511	4	US-10-099-285A-88	Sequence 88, Appl
293	85.5	4.8	789	4	US-10-099-285A-94	Sequence 94, Appl	366	82.5	4.7	789	3	US-09-002-285-82	Sequence 82, Appl
294	85.5	4.8	789	4	US-10-099-285A-100	Sequence 100, Appl	367	82.5	4.7	789	3	US-09-002-285-84	Sequence 84, Appl
295	85.5	4.8	790	3	US-08-960-780-8	Sequence 8, Appl	368	82.5	4.7	789	3	US-09-002-285-92	Sequence 92, Appl
296	85.5	4.8	790	3	US-09-073-898-8	Sequence 8, Appl	369	82.5	4.7	789	4	US-09-589-477-82	Sequence 82, Appl
297	85.5	4.8	790	4	US-09-307-106-2	Sequence 2, Appl	370	82.5	4.7	789	4	US-09-589-477-84	Sequence 84, Appl
298	85.5	4.8	790	4	US-09-850-351A-8	Sequence 8, Appl	371	82.5	4.7	789	4	US-09-589-477-92	Sequence 92, Appl
299	85.5	4.8	2491	4	US-09-207-363-1	Sequence 1, Appl	372	82.5	4.7	789	4	US-10-099-285A-82	Sequence 82, Appl
300	85	4.8	239	4	US-09-828-995B-26	Sequence 26, Appl	373	82.5	4.7	789	4	US-10-099-285A-84	Sequence 84, Appl
301	85	4.8	512	4	US-08-999-689A-7	Sequence 7, Appl	374	82.5	4.7	789	4	US-10-099-285A-92	Sequence 92, Appl
302	85	4.8	757	3	US-08-434-000A-6	Sequence 6, Appl	375	82.5	4.7	789	4	US-10-099-285A-102	Sequence 102, App
303	85	4.8	757	3	US-09-312-157-6	Sequence 6, Appl	376	82.5	4.7	790	4	US-09-589-477-102	Sequence 102, App
304	85	4.8	757	4	US-09-717-888-6	Sequence 6, Appl	377	82.5	4.7	790	4	US-10-099-285A-102	Sequence 102, App
305	85	4.8	821	4	US-09-622-880B-15	Sequence 15, Appl	378	82	4.6	314	4	US-09-107-532A-4919	Sequence 4919, Ap
306	84.5	4.8	175	4	US-09-869-388-8	Sequence 8, Appl	379	82	4.6	370	4	US-09-248-796A-18365	Sequence 18365, A
307	84.5	4.8	303	3	US-08-985-950-2	Sequence 2, Appl	380	82	4.6	449	3	US-09-118-319-7	Sequence 7, Appl
308	84.5	4.8	303	4	US-09-546-049-2	Sequence 2, Appl	381	82	4.6	449	3	US-09-286-691-4	Sequence 4, Appl
309	84.5	4.8	303	4	US-09-869-388-2	Sequence 2, Appl	382	82	4.6	449	3	US-09-687-147-4	Sequence 4, Appl
310	84	4.7	218	4	US-09-451-291-12	Sequence 12, Appl	383	82	4.6	567	4	US-09-773-877B-20	Sequence 20, Appl
311	84	4.7	339	4	US-09-719-243-2	Sequence 2, Appl	384	82	4.6	757	4	US-03-622-880B-1	Sequence 1, Appl
312	84	4.7	351	4	US-09-756-983-18	Sequence 18, Appl	385	82	4.6	874	2	US-08-456-647B-6	Sequence 6, Appl
313	84	4.7	358	4	US-09-719-243-3	Sequence 3, Appl	386	82	4.6	874	2	US-08-237-401A-6	Sequence 6, Appl
314	84	4.7	668	1	US-08-530-950-13	Sequence 13, Appl	387	82	4.6	880	1	US-08-445-640-10	Sequence 10, Appl
315	84	4.7	668	3	US-09-149-879-13	Sequence 13, Appl	388	82	4.6	880	3	US-08-170-558-10	Sequence 10, Appl
316	84	4.7	668	4	US-09-057-009-13	Sequence 13, Appl	389	82	4.6	880	3	US-08-447-314-10	Sequence 10, Appl
317	83.5	4.7	260	4	US-09-254-465A-23	Sequence 23, Appl	390	82	4.6	880	3	US-08-445-461-10	Sequence 10, Appl
318	83.5	4.7	260	4	US-09-953-499-23	Sequence 23, Appl	391	82	4.6	880	4	US-09-223-490-10	Sequence 10, Appl
319	83.5	4.7	263	4	US-09-254-465A-25	Sequence 25, Appl	392	82	4.6	1248	4	US-09-949-016-10595	Sequence 10595, A

393	82	4.6	1248	4	US-09-949-016-10596	Sequence 10596, A	466	79.5	4.5	859	4	US-09-708-200-7	Sequence 7, Appli
394	81.5	4.6	309	4	US-09-667-135-6	Sequence 6, Appli	467	79.5	4.5	859	4	US-09-788-657-16	Sequence 16, Appli
395	81.5	4.6	309	4	US-09-910-1748-7	Sequence 7, Appli	468	79.5	4.5	859	4	US-09-712-691-5	Sequence 5, Appli
396	81.5	4.6	309	4	US-09-620-461-7	Sequence 7, Appli	469	79	4.5	859	4	US-09-707-468C-5	Sequence 5, Appli
397	81.5	4.6	504	4	US-09-949-016-7020	Sequence 7020, Ap	470	78.5	4.4	393	1	US-08-429-742-2	Sequence 2, Appli
398	81.5	4.6	511	4	US-09-949-016-10054	Sequence 10054, A	471	78.5	4.4	439	3	US-09-383-586-32	Sequence 32, Appli
399	81.5	4.6	558	4	US-09-667-135-31	Sequence 31, Appli	472	78.5	4.4	439	4	US-09-047-026A-4	Sequence 4, Appli
400	81.5	4.6	846	1	US-08-149-103-4	Sequence 4, Appli	473	78.5	4.4	831	2	US-09-823-038A-32	Sequence 32, Appli
401	81.5	4.6	846	1	US-08-451-883-4	Sequence 4, Appli	474	79.5	4.4	857	4	US-09-248-796A-20522	Sequence 20522, A
402	81.5	4.6	1441	4	US-09-949-016-10397	Sequence 10397, A	475	78	4.4	341	1	US-08-248-628A-2	Sequence 2, Appli
403	81	4.6	144	6	5169835-8	Patent No. 5169835	476	78	4.4	345	4	US-09-214-631-5	Sequence 5, Appli
404	81	4.6	144	6	5169835-8	Patent No. 5169835	477	78	4.4	345	4	US-09-214-631-5	Sequence 5, Appli
405	81	4.6	252	2	US-08-414-657D-56	Sequence 56, Appli	478	78	4.4	588	4	US-09-949-016-10547	Sequence 10547, A
406	81	4.6	287	2	US-08-414-657D-48	Sequence 48, Appli	479	78	4.4	624	2	US-08-642-406A-22	Sequence 22, Appli
407	81	4.6	304	2	US-08-414-657D-44	Sequence 44, Appli	480	78	4.4	624	3	US-09-199-534-22	Sequence 22, Appli
408	81	4.6	308	2	US-08-414-657D-46	Sequence 46, Appli	481	78	4.4	624	4	US-09-199-534-22	Sequence 22, Appli
409	81	4.6	325	2	US-08-414-657D-2	Sequence 2, Appli	482	78	4.4	655	4	US-09-248-796A-14308	Sequence 14308, A
410	81	4.6	325	2	US-08-414-657D-41	Sequence 41, Appli	483	78	4.4	833	4	US-09-949-016-11496	Sequence 11496, A
411	81	4.6	325	4	US-09-135-080-2	Sequence 2, Appli	484	77.5	4.4	1180	4	US-09-949-016-6577	Sequence 6577, Ap
412	81	4.6	338	2	US-08-414-657D-60	Sequence 60, Appli	485	77.5	4.4	321	4	US-09-254-465A-2	Sequence 2, Appli
413	81	4.6	338	4	US-09-135-080-8	Sequence 8, Appli	486	77.5	4.4	477	2	US-09-533-499-2	Sequence 2, Appli
414	81	4.6	338	4	US-09-976-594-404	Sequence 404, App	487	77.5	4.4	477	2	US-08-432-016-3	Sequence 3, Appli
415	80.5	4.5	205	3	US-09-134-001C-4766	Sequence 4766, Ap	488	77.5	4.4	650	3	US-08-684-594-3	Sequence 3, Appli
416	80.5	4.5	313	4	US-09-701-623C-3	Sequence 3, Appli	489	77.5	4.4	650	4	US-09-310-463-2	Sequence 2, Appli
417	80.5	4.5	346	1	US-08-213-403-2	Sequence 2, Appli	490	77.5	4.4	662	1	US-08-842-248A-2	Sequence 2, Appli
418	80.5	4.5	346	1	US-08-458-077-2	Sequence 2, Appli	491	77.5	4.4	662	1	US-08-261-304-7	Sequence 7, Appli
419	80.5	4.5	346	1	US-08-460-741-2	Sequence 2, Appli	492	77.5	4.4	735	5	PCT-US93-00031-13	Sequence 13, Appli
420	80.5	4.5	346	1	US-08-747-240-2	Sequence 2, Appli	493	77.5	4.4	735	5	PCT-US93-00031-15	Sequence 15, Appli
421	80.5	4.5	346	1	US-08-299-567-6	Sequence 6, Appli	494	77.5	4.4	739	3	US-08-482-073-6	Sequence 6, Appli
422	80.5	4.5	346	1	US-09-039-642B-2	Sequence 2, Appli	495	77.5	4.4	739	5	PCT-US93-00031-9	Sequence 9, Appli
423	80.5	4.5	346	4	US-08-635-130A-9	Sequence 9, Appli	496	77.5	4.4	757	4	US-09-538-092-520	Sequence 520, App
424	80.5	4.5	522	4	US-09-949-016-11189	Sequence 11189, A	497	77	4.3	1312	4	US-09-554-572-36	Sequence 26, Appli
425	80.5	4.5	650	1	US-08-121-713D-60	Sequence 60, Appli	498	77	4.3	278	3	US-09-570-367C-2	Sequence 2, Appli
426	80.5	4.5	650	2	US-08-835-268-60	Sequence 60, Appli	499	77	4.3	278	4	US-09-915-524-2	Sequence 2, Appli
427	80.5	4.5	650	2	US-09-060-692-60	Sequence 60, Appli	500	77	4.3	278	4	US-09-934-634-2	Sequence 2, Appli
428	80.5	4.5	650	3	US-08-833-391-60	Sequence 60, Appli	501	77	4.3	362	4	US-09-291-299A-6	Sequence 6, Appli
429	80.5	4.5	650	3	US-09-060-610-60	Sequence 60, Appli	502	77	4.3	458	4	US-09-435-956A-1	Sequence 1, Appli
430	80.5	4.5	650	3	PCT-US94-10151A-60	Sequence 60, Appli	503	77	4.3	470	4	US-09-291-299A-1	Sequence 1, Appli
431	80.5	4.5	721	3	US-09-390-234-20	Sequence 20, Appli	504	77	4.3	476	4	US-09-291-299A-3	Sequence 3, Appli
432	80.5	4.5	721	4	US-09-603-311-20	Sequence 20, Appli	505	77	4.3	523	3	US-08-948-564-8	Sequence 8, Appli
433	80.5	4.5	789	3	US-08-960-780-6	Sequence 6, Appli	506	77	4.3	585	4	US-09-270-767-42396	Sequence 42396, A
434	80.5	4.5	789	3	US-09-073-898-6	Sequence 6, Appli	507	77	4.3	651	4	US-09-270-767-44877	Sequence 44877, A
435	80.5	4.5	828	1	US-08-261-304-2	Sequence 2, Appli	508	77	4.3	1021	1	US-08-497-025-3	Sequence 3, Appli
436	80.5	4.5	227	4	US-09-869-388-6	Sequence 6, Appli	509	77	4.3	1033	4	US-09-252-991A-20611	Sequence 20611, A
437	80	4.5	227	2	US-08-414-657D-57	Sequence 57, Appli	510	76.5	4.3	392	4	US-09-424-783A-2	Sequence 2, Appli
438	80	4.5	252	4	US-08-414-657D-45	Sequence 45, Appli	511	76.5	4.3	392	4	US-09-800-729-175	Sequence 175, App
439	80	4.5	287	2	US-08-414-657D-49	Sequence 49, Appli	512	76.5	4.3	364	4	US-08-896-537A-3	Sequence 3, Appli
440	80	4.5	310	2	US-08-414-657D-45	Sequence 45, Appli	513	76.5	4.3	490	4	US-09-667-135-28	Sequence 28, Appli
441	80	4.5	315	2	US-08-414-657D-47	Sequence 47, Appli	514	76.5	4.3	589	4	US-09-866-510-12	Sequence 12, Appli
442	80	4.5	338	2	US-08-414-657D-42	Sequence 42, Appli	515	76.5	4.3	1088	4	US-09-961-403-4	Sequence 4, Appli
443	80	4.5	338	2	US-08-414-657D-43	Sequence 43, Appli	516	76.5	4.3	1089	1	US-08-180-195-36	Sequence 36, Appli
444	80	4.5	338	4	US-09-135-080-4	Sequence 4, Appli	517	76.5	4.3	1089	1	US-08-168-917-4	Sequence 4, Appli
445	80	4.5	499	4	US-09-252-991A-23328	Sequence 23328, A	518	76.5	4.3	1089	2	US-08-477-329-36	Sequence 36, Appli
446	80	4.5	528	4	US-09-010-147B-20	Sequence 20, Appli	519	76.5	4.3	1089	2	US-08-475-458-36	Sequence 36, Appli
447	80	4.5	529	3	US-09-383-586-31	Sequence 31, Appli	520	76.5	4.3	1089	2	US-08-460-510-4	Sequence 4, Appli
448	80	4.5	529	4	US-09-823-038A-31	Sequence 31, Appli	521	76.5	4.3	1089	3	US-08-460-490-4	Sequence 4, Appli
449	80	4.5	607	2	US-08-752-307B-12	Sequence 12, Appli	522	76.5	4.3	1089	3	US-08-980-400-36	Sequence 36, Appli
450	80	4.5	607	3	US-09-707-802-12	Sequence 12, Appli	523	76.5	4.3	1089	3	US-08-462-728-2	Sequence 2, Appli
451	80	4.5	607	3	US-09-991-326-12	Sequence 12, Appli	524	76.5	4.3	1089	3	US-09-583-459A-36	Sequence 36, Appli
452	80	4.5	1233	3	US-09-194-613-5	Sequence 5, Appli	525	76.5	4.3	1089	3	US-09-583-449A-36	Sequence 36, Appli
453	79.5	4.5	202	6	5189147-6	Patent No. 5189147	526	76.5	4.3	1089	3	US-09-435-059-36	Sequence 36, Appli
454	79.5	4.5	202	6	5189147-6	Patent No. 5189147	527	76.5	4.3	1089	3	US-08-461-917-2	Sequence 2, Appli
455	79.5	4.5	278	3	US-09-570-367C-21	Sequence 21, Appli	528	76.5	4.3	1089	4	US-08-464-436-2	Sequence 2, Appli
456	79.5	4.5	278	4	US-09-915-524-21	Sequence 21, Appli	529	76.5	4.3	1089	4	US-08-464-436-2	Sequence 2, Appli
457	79.5	4.5	278	4	US-09-934-634-21	Sequence 21, Appli	530	76.5	4.3	1089	4	US-09-769-987-2	Sequence 2, Appli
458	79.5	4.5	309	4	US-09-248-796A-20432	Sequence 20432, A	531	76.5	4.3	1089	4	US-09-866-510-2	Sequence 2, Appli
459	79.5	4.5	328	3	US-08-821-994-84	Sequence 84, Appli	532	76.5	4.3	1089	4	US-09-866-510-6	Sequence 6, Appli
460	79.5	4.5	335	4	US-09-489-039A-11298	Sequence 11298, A	533	76.5	4.3	1089	4	US-09-866-510-8	Sequence 8, Appli
461	79.5	4.5	374	3	US-08-821-994-68	Sequence 68, Appli	534	76.5	4.3	1089	4	US-09-866-510-10	Sequence 10, Appli
462	79.5	4.5	402	3	US-09-292-097-16	Sequence 16, Appli	535	76.5	4.3	1089	4	US-09-919-497-90	Sequence 90, Appli
463	79.5	4.5	402	4	US-09-933-561-16	Sequence 16, Appli	536	76.5	4.3	1089	4	US-09-866-510-10	Sequence 10, Appli
464	79.5	4.5	643	1	US-08-471-570-6	Sequence 6, Appli	537	76.5	4.3	1089	4	US-09-949-016-6703	Sequence 6703, Ap
465	79.5	4.5	769	1	US-08-471-570-8	Sequence 8, Appli	538	76.5	4.3	1089	5	PCT-US92-00730-4	Sequence 4, Appli

539	76.5	4.3	1089	5	PCT-US92-00862-4	Sequence 4, Appli	612	74	4.2	1027	4	US-10-268-051-8	Sequence 8, Appli
540	76.5	4.3	1125	4	US-09-949-016-10194	Sequence 10194, A	613	74	4.2	1333	1	US-08-447-411-76	Sequence 76, Appl
541	76.5	4.3	1328	3	US-08-781-891-76	Sequence 76, Appl	614	74	4.2	1333	2	US-08-662-227-34	Sequence 34, Appl
542	76.5	4.3	1328	4	US-09-618-166-76	Sequence 166, Appl	615	74	4.2	1333	3	US-09-017-947-34	Sequence 34, Appl
543	76.5	4.3	1617	4	US-09-784-358-16	Sequence 16, Appl	616	74	4.2	1333	4	US-09-925-442-34	Sequence 34, Appl
544	76.5	4.3	1621	4	US-09-784-358-2	Sequence 2, Appli	617	74	4.2	1709	4	US-09-949-016-10503	Sequence 10503, A
545	76.5	4.3	1723	4	US-09-194-6128-31	Sequence 31, Appl	618	73.5	4.1	2179	3	US-09-134-001C-5638	Sequence 5638, Ap
546	76.5	4.3	1745	4	US-09-800-729-89	Sequence 89, Appl	619	73.5	4.1	238	3	US-08-978-289-10	Sequence 10, Appl
547	76	4.3	277	4	US-09-543-681A-4527	Sequence 4527, Ap	620	73.5	4.1	321	3	US-09-171-461-22	Sequence 22, Appl
548	76	4.3	378	1	US-08-225-477B-9	Sequence 9, Appli	621	73.5	4.1	321	4	US-09-970-711-22	Sequence 22, Appl
549	76	4.3	378	5	PCT-US95-04353-9	Sequence 9, Appli	622	73.5	4.1	334	4	US-09-248-796A-18143	Sequence 18143, A
550	76	4.3	390	3	US-08-961-564A-2	Sequence 2, Appli	623	73.5	4.1	334	4	US-09-700-397-3	Sequence 3, Appli
551	76	4.3	390	4	US-09-050-861B-2	Sequence 2, Appli	624	73.5	4.1	513	4	US-09-910-174B-18	Sequence 18, Appl
552	76	4.3	390	4	US-09-135-238B-2	Sequence 2, Appli	625	73.5	4.1	513	4	US-09-620-461-18	Sequence 18, Appl
553	76	4.3	462	4	US-09-773-877B-18	Sequence 18, Appl	626	73.5	4.1	611	3	US-09-248-796A-19450	Sequence 19450, A
554	76	4.3	463	3	US-09-082-310-1	Sequence 1, Appli	627	73.5	4.1	619	3	US-09-134-001C-4054	Sequence 4054, Ap
555	76	4.3	463	4	US-09-575-205-1	Sequence 1, Appli	628	73.5	4.1	716	3	US-09-171-945-125	Sequence 125, App
556	76	4.3	463	4	US-09-976-594-721	Sequence 721, App	629	73.5	4.1	842	4	US-09-902-540-11810	Sequence 11810, A
557	76	4.3	567	4	US-09-773-877B-12	Sequence 12, Appl	630	73.5	4.1	913	1	US-08-445-640-4	Sequence 4, Appli
558	76	4.3	599	1	US-08-442-542-18	Sequence 18, Appl	631	73.5	4.1	913	3	US-08-170-558-4	Sequence 4, Appli
559	76	4.3	599	3	US-08-765-469-18	Sequence 18, Appl	632	73.5	4.1	913	3	US-08-447-314-4	Sequence 4, Appli
560	76	4.3	759	4	US-09-902-540-16161	Sequence 16161, A	633	73.5	4.1	913	3	US-08-445-461-4	Sequence 4, Appli
561	75.5	4.3	446	4	US-09-583-110-4602	Sequence 4602, Ap	634	73.5	4.1	913	4	US-09-223-490-4	Sequence 4, Appli
562	75.5	4.3	448	4	US-09-107-433-3945	Sequence 3945, Ap	635	73.5	4.1	1000	3	US-09-193-562D-30	Sequence 30, Appl
563	75.5	4.3	514	4	US-10-142-231-68	Sequence 68, Appl	636	73.5	4.1	1000	4	US-10-055-412B-30	Sequence 30, Appl
564	75.5	4.3	530	4	US-09-949-016-9519	Sequence 9519, Ap	637	73.5	4.1	4544	1	US-08-469-486-52	Sequence 52, Appl
565	75.5	4.3	648	2	US-08-817-436A-2	Sequence 2, Appli	638	73.5	4.1	4544	2	US-08-469-486-52	Sequence 52, Appl
566	75	4.2	261	4	US-10-101-464A-691	Sequence 691, App	639	73	4.1	112	3	US-08-545-809A-136	Sequence 136, App
567	75	4.2	303	4	US-09-509-347-7	Sequence 7, Appli	640	73	4.1	155	4	US-09-270-767-57684	Sequence 57684, A
568	75	4.2	512	3	US-09-356-818A-2	Sequence 2, Appli	641	73	4.1	250	4	US-09-270-767-42724	Sequence 42724, A
569	75	4.2	527	4	US-09-910-174B-10	Sequence 10, Appl	642	73	4.1	270	4	US-09-563-611C-37	Sequence 37, Appl
570	75	4.2	527	4	US-09-620-461-10	Sequence 10, Appl	643	73	4.1	308	4	US-09-248-796A-14626	Sequence 14626, A
571	75	4.2	641	3	US-09-422-869-26	Sequence 26, Appl	644	73	4.1	373	4	US-08-823-038A-60	Sequence 60, Appl
572	75	4.2	762	4	US-09-949-016-7568	Sequence 7568, Ap	645	73	4.1	389	4	US-08-724-378D-3	Sequence 3, Appli
573	75	4.2	855	4	US-09-328-352-6216	Sequence 6216, Ap	646	73	4.1	459	1	US-08-157-101A-7	Sequence 7, Appli
574	75	4.2	1729	4	US-09-696-115B-2	Sequence 2, Appli	647	73	4.1	501	2	US-08-408-095-31	Sequence 31, Appl
575	75	4.2	2337	3	US-09-134-001C-4463	Sequence 4463, Ap	648	73	4.1	504	3	US-08-868-373-6	Sequence 6, Appli
576	74.5	4.2	218	3	US-09-068-653-7	Sequence 7, Appli	649	73	4.1	548	4	US-09-398-395A-12	Sequence 12, Appl
577	74.5	4.2	230	6	5169835-13	Patent No. 5169835	650	73	4.1	548	4	US-09-887-586A-12	Sequence 12, Appl
578	74.5	4.2	230	6	5169835-13	Patent No. 5169835	651	73	4.1	548	4	US-09-895-752-12	Sequence 12, Appl
579	74.5	4.2	338	4	US-09-688-188B-152	Sequence 152, App	652	73	4.1	548	4	US-09-903-012B-12	Sequence 12, Appl
580	74.5	4.2	338	4	US-09-291-417D-152	Sequence 97, Appl	653	73	4.1	548	4	US-09-900-797-12	Sequence 12, Appl
581	74.5	4.2	373	4	US-09-688-188B-97	Sequence 97, Appl	654	73	4.1	623	4	US-09-949-016-11206	Sequence 11206, A
582	74.5	4.2	373	4	US-09-291-417D-97	Sequence 67, Appl	655	73	4.1	646	4	US-09-653-961-2	Sequence 2, Appli
583	74.5	4.2	374	3	US-08-821-994-69	Sequence 69, Appl	656	73	4.1	651	3	US-08-985-950-22	Sequence 22, Appl
584	74.5	4.2	374	3	US-08-821-994-69	Sequence 69, Appl	657	73	4.1	651	4	US-09-546-049-22	Sequence 22, Appl
585	74.5	4.2	463	4	US-08-853-659A-52	Sequence 52, Appl	658	72.5	4.1	283	4	US-09-248-796A-19610	Sequence 19610, A
586	74.5	4.2	640	4	US-09-949-016-7565	Sequence 7565, Ap	659	72.5	4.1	293	6	5189147-3	Patent No. 5189147
587	74.5	4.2	789	3	US-09-002-283-98	Sequence 98, Appl	660	72.5	4.1	293	6	5189147-3	Patent No. 5189147
588	74.5	4.2	789	4	US-09-589-477-98	Sequence 98, Appl	661	72.5	4.1	331	1	US-08-364-081-3	Sequence 3, Appli
589	74.5	4.2	789	4	US-10-099-285A-98	Sequence 98, Appl	662	72.5	4.1	331	1	US-08-630-552-3	Sequence 3, Appli
590	74.5	4.2	1148	1	US-08-452-052-2	Sequence 2, Appli	663	72.5	4.1	331	5	PCT-US95-16558-3	Sequence 3, Appli
591	74.5	4.2	1148	2	US-08-313-185-58	Sequence 58, Appl	664	72.5	4.1	347	4	US-09-667-135-4	Sequence 4, Appli
592	74.5	4.2	1148	2	US-09-082-614A-58	Sequence 58, Appl	665	72.5	4.1	354	6	5169835-4	Patent No. 5169835
593	74.5	4.2	1788	3	US-08-962-284-2	Sequence 2, Appli	666	72.5	4.1	354	6	5169835-4	Patent No. 5169835
594	74.5	4.2	1911	1	US-08-348-006B-5	Sequence 5, Appli	667	72.5	4.1	374	3	US-08-821-994-70	Sequence 70, Appl
595	74.5	4.2	1911	2	US-08-800-825A-5	Sequence 5, Appli	668	72.5	4.1	390	2	US-08-979-424-1	Sequence 1, Appli
596	74.5	4.2	1911	3	US-09-158-657-5	Sequence 5, Appli	669	72.5	4.1	390	4	US-09-907-794A-39	Sequence 39, Appl
597	74.5	4.2	454	5	PCT-US94-10166-5	Sequence 5, Appli	670	72.5	4.1	390	4	US-09-905-125A-39	Sequence 39, Appl
598	74.5	4.2	454	3	US-08-476-515A-84	Sequence 84, Appl	671	72.5	4.1	390	4	US-09-902-775A-39	Sequence 39, Appl
599	74.5	4.2	455	3	US-08-652-877-84	Sequence 84, Appl	672	72.5	4.1	390	4	US-09-906-700-39	Sequence 39, Appl
600	74.5	4.2	455	3	US-08-652-877-84	Sequence 86, Appl	673	72.5	4.1	390	4	US-09-903-603A-39	Sequence 39, Appl
601	74.5	4.2	455	3	US-08-652-877-88	Sequence 88, Appl	674	72.5	4.1	390	4	US-09-904-920A-39	Sequence 39, Appl
602	74.5	4.2	455	3	US-08-652-877-90	Sequence 90, Appl	675	72.5	4.1	390	4	US-09-909-064-39	Sequence 39, Appl
603	74	4.2	343	3	US-09-454-034-8	Sequence 8, Appli	676	72.5	4.1	390	4	US-09-905-381A-39	Sequence 39, Appl
604	74	4.2	387	3	US-09-175-928-2	Sequence 2, Appli	677	72.5	4.1	390	4	US-09-906-618-39	Sequence 39, Appl
605	74	4.2	451	4	US-09-107-532A-6652	Sequence 6652, Ap	678	72.5	4.1	424	6	5169835-6	Patent No. 5169835
606	74	4.2	543	4	US-09-042-709A-18	Sequence 18, Appl	679	72.5	4.1	424	6	5169835-6	Patent No. 5169835
607	74	4.2	548	1	US-08-247-902A-2	Sequence 2, Appli	680	72.5	4.1	489	3	US-09-134-001C-4902	Sequence 4902, Ap
608	74	4.2	548	5	PCT-US93-10541-2	Sequence 2, Appli	681	72.5	4.1	521	2	US-08-504-048-9	Sequence 9, Appli
609	74	4.2	705	4	US-09-949-016-10140	Sequence 10140, A	682	72.5	4.1	526	1	US-08-471-570-4	Sequence 4, Appli
610	74	4.2	862	4	US-08-556-422A-2	Sequence 2, Appli	683	72.5	4.1	560	4	US-09-071-035-220	Sequence 220, App
611	74	4.2	1027	3	US-09-162-021B-2	Sequence 2, Appli	684	72.5	4.1	605	2	US-08-753-307B-8	Sequence 8, Appli

685	72.5	4.1	605	3	US-09-707-802-8	Sequence 8, Appli	758	71.5	4.0	206	3	US-08-821-994-77	Sequence 77, Appli
686	72.5	4.1	605	3	US-09-991-326-8	Sequence 8, Appli	759	71.5	4.0	241	4	US-09-248-796A-17942	Sequence 17942, A
687	72.5	4.1	627	4	US-09-071-035-218	Sequence 218, App	760	71.5	4.0	248	6	5169835-15	Patent No. 5169835
688	72.5	4.1	635	4	US-10-101-464A-932	Sequence 932, App	761	71.5	4.0	248	6	5169835-15	Patent No. 5169835
689	72.5	4.1	652	1	US-08-471-570-10	Sequence 10, Appl	762	71.5	4.0	327	3	US-09-173-581-5	Sequence 5, Appli
690	72.5	4.1	659	4	US-09-134-000C-6124	Sequence 6124, Ap	763	71.5	4.0	327	3	US-08-420-915-5	Sequence 5, Appli
691	72.5	4.1	759	3	US-09-002-285-86	Sequence 86, Appl	764	71.5	4.0	384	4	US-09-552-322-2	Sequence 2, Appli
692	72.5	4.1	759	4	US-09-589-477-86	Sequence 86, Appl	765	71.5	4.0	403	4	US-09-638-649-5	Sequence 5, Appli
693	72.5	4.1	759	4	US-10-099-285A-86	Sequence 86, Appl	766	71.5	4.0	403	4	US-09-638-649-5	Sequence 5, Appli
694	72.5	4.1	768	4	US-09-489-039A-12897	Sequence 12897, A	767	71.5	4.0	456	4	US-09-638-648-5	Sequence 23791, A
695	72.5	4.1	790	4	US-09-543-681A-5459	Sequence 5459, Ap	768	71.5	4.0	456	4	US-09-248-796A-23791	Sequence 18, Appl
696	72.5	4.1	913	4	US-09-140-378A-2	Sequence 2, Appli	769	71.5	4.0	462	4	US-09-166-350-18	Sequence 11, Appl
697	72.5	4.1	919	1	US-08-336-343A-2	Sequence 2, Appli	770	71.5	4.0	523	4	US-09-910-174B-11	Sequence 11, Appl
698	72.5	4.1	937	4	US-09-949-016-8366	Sequence 8366, Ap	771	71.5	4.0	523	4	US-09-620-461-11	Sequence 4, Appli
699	72.5	4.1	937	4	US-09-949-016-8367	Sequence 8367, Ap	772	71.5	4.0	608	3	US-09-095-385-4	Sequence 4, Appli
700	72.5	4.1	937	4	US-09-949-016-8368	Sequence 8368, Ap	773	71.5	4.0	624	4	US-09-949-016-10587	Sequence 10587, A
701	72.5	4.1	1434	2	US-09-540-408-10	Sequence 10, Appl	774	71.5	4.0	624	4	US-09-434-000A-4	Sequence 4, Appli
702	72.5	4.1	1434	3	US-08-656-055-10	Sequence 10, Appl	775	71.5	4.0	746	3	US-09-312-157-4	Sequence 4, Appli
703	72.5	4.1	1434	3	US-08-954-668-10	Sequence 10, Appl	776	71.5	4.0	746	4	US-09-717-888-4	Sequence 4, Appli
704	72.5	4.1	1434	4	US-08-918-658-10	Sequence 10, Appl	777	71.5	4.0	764	4	US-09-949-016-6254	Sequence 6254, Ap
705	72.5	4.1	1434	4	US-09-724-631-10	Sequence 10, Appl	778	71.5	4.0	816	4	US-09-949-016-8119	Sequence 8119, Ap
706	72.5	4.1	1434	4	US-08-954-701A-10	Sequence 10, Appl	779	71.5	4.0	919	2	US-08-788-674-4	Sequence 4, Appli
707	72.5	4.1	1434	5	PCT-US95-13233-10	Sequence 10, Appl	780	71.5	4.0	941	4	US-09-949-016-6062	Sequence 6062, Ap
708	72	4.1	222	4	US-09-248-796A-20974	Sequence 20974, A	781	71.5	4.0	1006	4	US-09-949-016-10730	Sequence 10730, A
709	72	4.1	311	4	US-09-252-991A-28792	Sequence 28792, A	782	71.5	4.0	1255	4	US-09-902-540-12628	Sequence 12628, A
710	72	4.1	328	4	US-09-489-039A-13216	Sequence 13216, A	783	71.5	4.0	1405	4	US-09-248-796A-18103	Sequence 18103, A
711	72	4.1	348	2	US-09-031-485-28	Sequence 28, Appl	784	71.5	4.0	2468	4	US-09-976-594-726	Sequence 726, App
712	72	4.1	348	2	US-08-847-429A-28	Sequence 28, Appl	785	71.5	4.0	2468	4	US-09-538-092-1135	Sequence 1135, Ap
713	72	4.1	348	3	US-09-065-474-28	Sequence 28, Appl	786	71	4.0	2522	4	US-09-949-016-10237	Sequence 10237, A
714	72	4.1	348	3	US-09-557-034-28	Sequence 28, Appl	787	71	4.0	107	1	US-08-425-336-125	Sequence 125, App
715	72	4.1	358	4	US-09-265-585C-118	Sequence 118, App	788	71	4.0	107	1	US-08-488-113B-125	Sequence 125, App
716	72	4.1	379	4	US-09-265-585C-109	Sequence 109, App	789	71	4.0	107	1	US-08-477-484B-65	Sequence 65, Appl
717	72	4.1	379	3	US-09-186-276B-46	Sequence 46, Appl	790	71	4.0	107	1	US-08-472-788A-87	Sequence 87, Appl
718	72	4.1	379	4	US-08-842-445-46	Sequence 46, Appl	791	71	4.0	107	2	US-08-477-831B-65	Sequence 65, Appl
719	72	4.1	379	4	US-09-186-188B-46	Sequence 46, Appl	792	71	4.0	107	2	US-08-646-360-125	Sequence 125, App
720	72	4.1	394	4	US-09-265-585C-46	Sequence 46, Appl	793	71	4.0	107	2	US-08-082-842A-87	Sequence 87, Appl
721	72	4.1	394	4	US-09-949-016-6716	Sequence 6716, Ap	794	71	4.0	107	3	US-08-839-765-125	Sequence 125, App
722	72	4.1	427	4	US-09-949-016-9842	Sequence 9842, Ap	795	71	4.0	107	3	US-08-839-765-125	Sequence 125, App
723	72	4.1	452	4	US-09-773-877B-16	Sequence 16, Appl	796	71	4.0	107	3	US-09-610-838-125	Sequence 125, App
724	72	4.1	456	1	US-08-435-933-6	Sequence 6, Appli	797	71	4.0	107	4	US-09-711-485-125	Sequence 125, App
725	72	4.1	456	5	PCT-US96-06035-6	Sequence 6, Appli	798	71	4.0	233	4	US-09-198-452A-244	Sequence 244, App
726	72	4.1	497	3	US-08-709-731A-29	Sequence 29, Appl	799	71	4.0	233	4	US-09-438-185A-236	Sequence 236, App
727	72	4.1	514	4	US-09-949-016-11380	Sequence 11380, A	800	71	4.0	236	3	US-09-049-672A-7	Sequence 7, Appli
728	72	4.1	517	4	US-09-723-368-4	Sequence 4, Appli	801	71	4.0	240	1	US-08-488-113B-147	Sequence 147, App
729	72	4.1	528	4	US-09-710-279-1930	Sequence 1930, Ap	802	71	4.0	240	1	US-08-488-113B-148	Sequence 148, App
730	72	4.1	548	4	US-09-398-395A-2	Sequence 2, Appli	803	71	4.0	240	1	US-08-477-484B-147	Sequence 147, App
731	72	4.1	548	4	US-09-887-588A-2	Sequence 2, Appli	804	71	4.0	240	1	US-08-477-484B-148	Sequence 148, App
732	72	4.1	548	4	US-09-895-752-2	Sequence 2, Appli	805	71	4.0	240	2	US-08-646-360-147	Sequence 147, App
733	72	4.1	548	4	US-09-903-012B-2	Sequence 2, Appli	806	71	4.0	240	2	US-08-646-360-148	Sequence 148, App
734	72	4.1	548	4	US-09-900-797-2	Sequence 14, Appli	807	71	4.0	240	3	US-08-839-765-147	Sequence 147, App
735	72	4.1	557	4	US-09-773-877B-14	Sequence 14, Appl	808	71	4.0	240	3	US-08-839-765-148	Sequence 148, App
736	72	4.1	633	4	US-09-248-796A-20407	Sequence 20407, A	809	71	4.0	240	3	US-09-136-389-147	Sequence 147, App
737	72	4.1	646	4	US-09-949-016-6728	Sequence 6728, Ap	810	71	4.0	240	3	US-09-136-389-148	Sequence 148, App
738	72	4.1	646	4	US-09-653-961-4	Sequence 4, Appli	811	71	4.0	240	3	US-09-610-838-147	Sequence 147, App
739	72	4.1	670	4	US-09-575-081B-27	Sequence 27, Appl	812	71	4.0	240	3	US-09-610-838-148	Sequence 148, App
740	72	4.1	670	4	US-09-949-016-6584	Sequence 6584, Ap	813	71	4.0	240	3	US-09-610-838-148	Sequence 148, App
741	72	4.1	670	4	US-09-949-016-6990	Sequence 6990, Ap	814	71	4.0	240	4	US-09-711-485-148	Sequence 148, App
742	72	4.1	679	4	US-09-949-016-8034	Sequence 8034, Ap	815	71	4.0	240	4	US-09-543-681A-7089	Sequence 7089, Ap
743	72	4.1	679	4	US-09-949-016-8035	Sequence 8035, Ap	816	71	4.0	379	4	US-09-543-681A-7089	Sequence 2, Appli
744	72	4.1	754	2	US-08-525-864A-2	Sequence 2, Appli	817	71	4.0	384	4	US-08-504-617-2	Sequence 11, Appl
745	72	4.1	852	4	US-09-319-588C-18	Sequence 18, Appl	818	71	4.0	475	3	US-08-657-749D-11	Sequence 11, Appl
746	72	4.1	1297	3	US-09-540-245A-17	Sequence 17, Appl	819	71	4.0	615	3	US-09-297-937C-9	Sequence 9, Appli
747	72	4.1	1456	1	US-08-803-973-2	Sequence 2, Appli	820	71	4.0	621	4	US-09-248-796A-14463	Sequence 14463, A
748	72	4.1	1456	1	US-08-803-972-2	Sequence 2, Appli	821	71	4.0	621	4	US-08-753-007A-32	Sequence 32, Appl
749	72	4.1	1456	2	US-09-031-485-33	Sequence 33, Appl	822	71	4.0	647	3	US-09-398-496-32	Sequence 32, Appl
750	72	4.1	1745	2	US-08-847-429A-33	Sequence 33, Appl	823	71	4.0	661	2	US-08-233-538-12	Sequence 12, Appl
751	72	4.1	1745	3	US-09-065-474-33	Sequence 33, Appl	824	71	4.0	661	2	US-08-233-538-12	Sequence 12, Appl
752	72	4.1	1745	3	US-09-557-034-33	Sequence 33, Appl	825	71	4.0	687	1	US-08-786-164-6	Sequence 6, Appli
753	72	4.1	2383	4	US-09-492-709A-302	Sequence 302, App	826	71	4.0	687	3	US-09-427-353-2	Sequence 2, Appli
754	72	4.1	2553	4	US-09-949-016-7659	Sequence 7659, Ap	827	71	4.0	731	4	US-09-107-532A-6999	Sequence 6999, Ap
755	72	4.1	2553	4	US-09-949-016-7660	Sequence 7660, Ap	828	71	4.0	758	2	US-08-874-678-1	Sequence 1, Appli
756	72	4.1	2870	4	US-10-220-587-2	Sequence 2, Appli	829	71	4.0	758	3	US-08-643-839-1	Sequence 1, Appli
757	72	4.1	4872	4	US-09-424-783-3	Sequence 3, Appli	830	71	4.0	758	3	US-09-051-363-24	Sequence 24, Appli



831	71	4.0	758	3	US-09-348-886-1	Sequence 1, Appli	904	70.5	4.0	1356	3	US-09-098-707A-2	Sequence 2, Appli
832	71	4.0	780	1	US-08-232-538-14	Sequence 14, Appl	905	70.5	4.0	1356	3	US-09-483-539-2	Sequence 2, Appli
833	71	4.0	780	2	US-08-786-164-14	Sequence 14, Appl	906	70.5	4.0	1356	3	US-09-949-016-6198	Sequence 6198, Ap
834	71	4.0	821	2	US-08-451-822A-13	Sequence 13, Appl	907	70.5	4.0	1456	3	US-09-949-016-9853	Sequence 9853, Ap
835	71	4.0	821	3	US-08-323-430-13	Sequence 13, Appl	908	70.5	4.0	126	3	US-09-240-274-146	Sequence 146, App
836	71	4.0	906	3	US-09-650-855-13	Sequence 13, Appl	909	70	4.0	167	3	US-08-821-994-43	Sequence 43, Appl
837	71	4.0	906	3	US-09-651-855-13	Sequence 13, Appl	910	70	4.0	282	3	US-09-602-787A-162	Sequence 162, App
838	71	4.0	916	4	US-09-919-497-64	Sequence 64, Appl	911	70	4.0	282	4	US-09-602-787A-164	Sequence 164, App
839	71	4.0	930	3	US-09-134-001C-5314	Sequence 5314, Ap	912	70	4.0	313	4	US-09-252-991A-32836	Sequence 32836, A
840	71	4.0	930	4	US-09-386-962C-10	Sequence 10, Appl	913	70	4.0	320	3	US-09-036-987A-14	Sequence 14, Appl
841	71	4.0	975	4	US-09-695-481-4	Sequence 4, Appli	914	70	4.0	320	3	US-09-370-700-14	Sequence 14, Appl
842	71	4.0	1018	1	US-08-408-093-6	Sequence 6, Appli	915	70	4.0	320	3	US-09-603-207-14	Sequence 14, Appl
843	71	4.0	1018	1	US-08-408-420A-6	Sequence 6, Appli	916	70	4.0	338	1	US-08-442-043A-17	Sequence 17, Appl
844	71	4.0	1018	1	US-08-714-901-6	Sequence 6, Appli	917	70	4.0	338	4	US-08-441-893A-17	Sequence 17, Appl
845	71	4.0	1018	3	US-08-040-741-6	Sequence 6, Appli	918	70	4.0	347	1	US-07-940-861-43	Sequence 43, Appl
846	71	4.0	1044	4	US-09-949-016-10321	Sequence 10321, A	919	70	4.0	347	1	US-08-459-512-43	Sequence 43, Appl
847	71	4.0	1082	4	US-09-538-092-533	Sequence 533, App	920	70	4.0	347	2	US-08-459-657-43	Sequence 43, Appl
848	71	4.0	1276	3	US-09-297-937C-13	Sequence 13, Appl	921	70	4.0	347	2	US-08-460-132-43	Sequence 43, Appl
849	71	4.0	1338	3	US-08-750-141A-3	Sequence 3, Appli	922	70	4.0	347	3	US-08-466-465-8	Sequence 8, Appli
850	71	4.0	1338	4	US-09-119-014D-6	Sequence 6, Appli	923	70	4.0	347	4	US-09-730-465-8	Sequence 8, Appli
851	71	4.0	1362	2	US-08-874-678-33	Sequence 33, Appl	924	70	4.0	347	5	PCT-US92-02050-43	Sequence 43, Appl
852	71	4.0	1362	3	US-08-643-839-33	Sequence 33, Appl	925	70	4.0	363	4	US-09-949-016-11040	Sequence 11040, A
853	71	4.0	1362	3	US-09-348-886-33	Sequence 33, Appl	926	70	4.0	412	4	US-09-543-681A-5782	Sequence 5782, Ap
854	71	4.0	1481	2	US-08-616-844-40	Sequence 40, Appl	927	70	4.0	469	3	US-08-753-007A-8	Sequence 8, Appli
855	71	4.0	1481	2	US-08-599-654-40	Sequence 40, Appl	928	70	4.0	469	3	US-09-398-496-8	Sequence 8, Appli
856	71	4.0	1481	3	US-08-944-868A-40	Sequence 40, Appl	929	70	4.0	490	4	US-09-489-039A-9610	Sequence 9610, Ap
857	71	4.0	1481	3	US-08-944-423A-40	Sequence 40, Appl	930	70	4.0	523	4	US-09-248-796A-17555	Sequence 17555, A
858	71	4.0	1481	3	US-08-944-496-40	Sequence 40, Appl	931	70	4.0	548	4	US-09-398-395A-6	Sequence 6, Appli
859	71	4.0	4391	4	US-10-006-011A-2	Sequence 2, Appli	932	70	4.0	548	4	US-09-398-395A-6	Sequence 6, Appli
860	70.5	4.0	183	4	US-09-621-976-3942	Sequence 3942, Ap	933	70	4.0	548	4	US-09-398-395A-8	Sequence 8, Appli
861	70.5	4.0	261	4	US-09-899-634C-2	Sequence 2, Appli	934	70	4.0	548	4	US-09-398-395A-10	Sequence 10, Appl
862	70.5	4.0	314	4	US-09-438-185A-452	Sequence 452, App	935	70	4.0	548	4	US-09-887-586A-4	Sequence 4, Appli
863	70.5	4.0	334	3	US-09-248-796A-15744	Sequence 15744, A	936	70	4.0	548	4	US-09-887-586A-6	Sequence 6, Appli
864	70.5	4.0	338	3	US-08-922-957-1	Sequence 1, Appli	937	70	4.0	548	4	US-09-887-586A-8	Sequence 8, Appli
865	70.5	4.0	338	3	US-08-922-957-3	Sequence 3, Appli	938	70	4.0	548	4	US-09-887-586A-10	Sequence 10, Appl
866	70.5	4.0	343	4	US-09-134-000C-6363	Sequence 6363, Ap	939	70	4.0	548	4	US-09-895-752-4	Sequence 4, Appli
867	70.5	4.0	371	4	US-09-248-796A-16428	Sequence 16428, A	940	70	4.0	548	4	US-09-895-752-6	Sequence 6, Appli
868	70.5	4.0	374	4	US-09-248-796A-15744	Sequence 15744, A	941	70	4.0	548	4	US-09-895-752-8	Sequence 8, Appli
869	70.5	4.0	466	3	US-09-134-001C-3526	Sequence 3526, Ap	942	70	4.0	548	4	US-09-895-752-10	Sequence 10, Appl
870	70.5	4.0	467	3	US-08-821-994-83	Sequence 83, Appl	943	70	4.0	548	4	US-09-903-012B-4	Sequence 4, Appli
871	70.5	4.0	472	4	US-09-710-279-1352	Sequence 1352, Ap	944	70	4.0	548	4	US-09-903-012B-6	Sequence 6, Appli
872	70.5	4.0	491	3	US-09-134-001C-4727	Sequence 4727, Ap	945	70	4.0	548	4	US-09-903-012B-8	Sequence 8, Appli
873	70.5	4.0	502	4	US-09-489-039A-8035	Sequence 8035, Ap	946	70	4.0	548	4	US-09-903-012B-10	Sequence 10, Appl
874	70.5	4.0	533	1	US-07-820-011A-2	Sequence 2, Appli	947	70	4.0	548	4	US-09-900-797-4	Sequence 4, Appli
875	70.5	4.0	533	4	US-09-470-881-3	Sequence 3, Appli	948	70	4.0	548	4	US-09-900-797-6	Sequence 6, Appli
876	70.5	4.0	533	5	PCT-US93-00445-2	Sequence 2, Appli	949	70	4.0	548	4	US-09-900-797-8	Sequence 8, Appli
877	70.5	4.0	579	3	US-09-173-151A-2	Sequence 2, Appli	950	70	4.0	548	4	US-09-900-797-10	Sequence 10, Appl
878	70.5	4.0	610	4	US-09-976-594-947	Sequence 947, App	951	70	4.0	550	2	US-08-443-639-8	Sequence 8, Appli
879	70.5	4.0	617	3	US-09-188-930-303	Sequence 303, App	952	70	4.0	550	3	US-08-577-483-8	Sequence 8, Appli
880	70.5	4.0	617	4	US-09-312-283C-303	Sequence 303, App	953	70	4.0	550	4	US-09-435-380-8	Sequence 8, Appli
881	70.5	4.0	644	4	US-09-949-016-11714	Sequence 11714, A	954	70	4.0	551	3	US-09-303-064-53	Sequence 53, Appl
882	70.5	4.0	668	1	US-08-232-538-13	Sequence 13, Appl	955	70	4.0	551	3	US-09-086-503-53	Sequence 53, Appl
883	70.5	4.0	668	2	US-08-786-164-13	Sequence 13, Appl	956	70	4.0	576	1	US-07-821-716-4	Sequence 4, Appli
884	70.5	4.0	686	3	US-09-173-151A-4	Sequence 4, Appli	957	70	4.0	576	2	US-08-381-603-4	Sequence 4, Appli
885	70.5	4.0	760	4	US-09-248-796A-17568	Sequence 17568, A	958	70	4.0	576	3	US-08-524-376-4	Sequence 4, Appli
886	70.5	4.0	764	3	US-09-142-956B-14	Sequence 14, Appl	959	70	4.0	576	3	US-08-685-212-4	Sequence 4, Appli
887	70.5	4.0	767	2	US-08-874-678-2	Sequence 2, Appli	960	70	4.0	576	3	US-09-173-151A-30	Sequence 30, Appl
888	70.5	4.0	767	3	US-08-643-839-2	Sequence 2, Appli	961	70	4.0	576	4	US-08-466-932A-4	Sequence 4, Appli
889	70.5	4.0	787	1	US-09-348-886-2	Sequence 2, Appli	962	70	4.0	576	5	PCT-US94-02414-4	Sequence 4, Appli
890	70.5	4.0	788	1	US-08-232-538-15	Sequence 15, Appl	963	70	4.0	582	4	US-09-147-405B-13	Sequence 13, Appl
891	70.5	4.0	788	2	US-08-786-164-15	Sequence 15, Appl	964	70	4.0	582	4	US-09-147-405B-13	Sequence 13, Appl
892	70.5	4.0	940	4	US-09-198-452A-500	Sequence 500, App	965	70	4.0	593	4	US-07-757-342D-8	Sequence 8, Appli
893	70.5	4.0	940	4	US-09-438-185A-468	Sequence 468, App	966	70	4.0	611	3	US-07-757-342D-8	Sequence 8, Appli
894	70.5	4.0	983	3	US-09-412-554A-2	Sequence 2, Appli	967	70	4.0	611	4	US-09-461-657B-8	Sequence 8, Appli
895	70.5	4.0	1088	1	US-08-485-588-6	Sequence 6, Appli	968	70	4.0	625	3	US-09-134-001C-4504	Sequence 4504, Ap
896	70.5	4.0	1088	1	US-08-484-565-6	Sequence 6, Appli	969	70	4.0	629	4	US-10-101-464A-927	Sequence 927, App
897	70.5	4.0	1088	2	US-08-480-751-6	Sequence 6, Appli	970	70	4.0	636	3	US-07-757-342D-7	Sequence 7, Appli
898	70.5	4.0	1088	2	US-08-943-986-6	Sequence 6, Appli	971	70	4.0	636	4	US-09-461-657B-7	Sequence 7, Appli
899	70.5	4.0	1088	3	US-08-353-784-6	Sequence 6, Appli	972	70	4.0	637	4	US-09-569-611C-35	Sequence 35, Appl
900	70.5	4.0	1088	3	US-08-484-719B-6	Sequence 6, Appli	973	70	4.0	652	3	US-09-310-463-4	Sequence 4, Appli
901	70.5	4.0	1088	3	US-08-484-159-6	Sequence 6, Appli	974	70	4.0	652	4	US-08-842-248A-4	Sequence 4, Appli
902	70.5	4.0	1356	1	US-08-810-116-8	Sequence 8, Appli	975	70	4.0	687	5	PCT-US91-09784-2	Sequence 2, Appli
903	70.5	4.0	1356	2	US-07-930-548A-8	Sequence 8, Appli	976	70	4.0	783	4	US-08-780-562-7	Sequence 7, Appli

977	70	4.0	837	1	US-07-923-976-2	Sequence 2, Appli	1050	69	3.9	360	3	US-08-875-811-47	Sequence 47, Appli
978	70	4.0	894	2	US-08-599-4558-2	Sequence 2, Appli	1051	69	3.9	379	3	US-08-875-811-43	Sequence 43, Appli
979	70	4.0	894	3	US-09-069-781B-2	Sequence 2, Appli	1052	69	3.9	383	4	US-09-079-030-82	Sequence 82, Appli
980	70	4.0	894	3	US-08-618-957A-12	Sequence 12, Appli	1053	69	3.9	408	4	US-09-248-796A-17517	Sequence 17517, A
981	70	4.0	894	3	US-09-137-132-2	Sequence 2, Appli	1054	69	3.9	467	4	US-08-030-175-42	Sequence 42, Appli
982	70	4.0	894	3	US-08-864-564A-2	Sequence 2, Appli	1055	69	3.9	468	1	US-08-220-151-16	Sequence 16, Appli
983	70	4.0	894	4	US-09-094-410-2	Sequence 2, Appli	1056	69	3.9	468	1	US-08-413-118-16	Sequence 16, Appli
984	70	4.0	894	4	US-08-708-123D-2	Sequence 2, Appli	1057	69	3.9	468	3	US-08-473-446-16	Sequence 16, Appli
985	70	4.0	894	4	US-08-583-153A-2	Sequence 2, Appli	1058	69	3.9	514	4	US-08-800-729-124	Sequence 124, App
986	70	4.0	894	4	US-08-570-142D-2	Sequence 2, Appli	1059	69	3.9	519	3	US-08-996-338-21	Sequence 21, Appli
987	70	4.0	894	4	US-08-638-524B-2	Sequence 2, Appli	1060	69	3.9	519	4	US-08-556-972-21	Sequence 21, Appli
988	70	4.0	894	4	US-10-095-923-12	Sequence 12, Appli	1061	69	3.9	523	3	US-08-606-505B-67	Sequence 67, Appli
989	70	4.0	944	3	US-09-449-285A-2	Sequence 2, Appli	1062	69	3.9	523	3	US-09-616-990-67	Sequence 67, Appli
990	70	4.0	950	3	US-09-449-285A-4	Sequence 4, Appli	1063	69	3.9	537	1	US-08-604-333-4	Sequence 4, Appli
991	70	4.0	1092	4	US-09-147-405B-15	Sequence 15, Appli	1064	69	3.9	537	3	US-09-110-618-4	Sequence 4, Appli
992	70	4.0	1162	2	US-08-599-455B-43	Sequence 43, Appli	1065	69	3.9	537	3	US-09-173-151A-29	Sequence 29, Appli
993	70	4.0	1162	3	US-09-069-781B-43	Sequence 43, Appli	1066	69	3.9	537	4	US-09-578-178-4	Sequence 4, Appli
994	70	4.0	1162	3	US-09-137-132-43	Sequence 43, Appli	1067	69	3.9	537	4	US-08-577-806-4	Sequence 4, Appli
995	70	4.0	1162	3	US-08-864-564A-43	Sequence 43, Appli	1068	69	3.9	537	4	US-09-621-502-8	Sequence 8, Appli
996	70	4.0	1162	4	US-09-094-410-43	Sequence 43, Appli	1069	69	3.9	542	1	US-08-140-729A-5	Sequence 5, Appli
997	70	4.0	1162	4	US-08-708-123D-43	Sequence 43, Appli	1070	69	3.9	542	1	US-08-546-666-5	Sequence 5, Appli
998	70	4.0	1162	4	US-08-638-524B-43	Sequence 43, Appli	1071	69	3.9	542	2	US-08-916-745-5	Sequence 5, Appli
999	70	4.0	1214	4	US-09-949-016-6885	Sequence 6885, Ap	1072	69	3.9	542	2	US-08-663-808-4	Sequence 4, Appli
1000	70	4.0	1318	4	US-09-949-016-7130	Sequence 7130, Ap	1073	69	3.9	542	2	US-08-042-929-5	Sequence 5, Appli
1001	70	4.0	2183	3	US-09-976-594-531	Sequence 531, Ap	1074	69	3.9	542	2	US-08-546-661-5	Sequence 5, Appli
1002	70	4.0	307	4	US-08-746-111-5	Sequence 5, Appli	1075	69	3.9	542	2	US-09-042-960-5	Sequence 5, Appli
1003	69.5	3.9	307	4	US-09-540-236-2790	Sequence 2790, Ap	1076	69	3.9	542	3	US-09-198-650-5	Sequence 5, Appli
1004	69.5	3.9	314	2	US-08-353-476-71	Sequence 71, Appli	1077	69	3.9	542	3	US-09-332-740-4	Sequence 4, Appli
1005	69.5	3.9	324	4	US-09-328-352-4577	Sequence 4577, Ap	1078	69	3.9	542	3	US-09-042-913-5	Sequence 5, Appli
1006	69.5	3.9	328	1	US-08-225-477B-5	Sequence 5, Appli	1079	69	3.9	542	3	US-09-188-436-4	Sequence 4, Appli
1007	69.5	3.9	328	5	PCR-US955-04353-5	Sequence 5, Appli	1080	69	3.9	542	3	US-09-042-937-5	Sequence 5, Appli
1008	69.5	3.9	333	1	US-08-436-463-6	Sequence 6, Appli	1081	69	3.9	542	3	US-09-368-282-4	Sequence 4, Appli
1009	69.5	3.9	333	1	US-08-024-253-6	Sequence 6, Appli	1082	69	3.9	542	4	US-09-566-708A-4	Sequence 4, Appli
1010	69.5	3.9	334	2	US-09-134-000C-5207	Sequence 5207, Ap	1083	69	3.9	542	4	US-09-042-709A-5	Sequence 5, Appli
1011	69.5	3.9	334	2	US-08-646-981-16	Sequence 16, Appli	1084	69	3.9	542	4	US-09-227-614-5	Sequence 5, Appli
1012	69.5	3.9	447	4	US-09-198-452A-972	Sequence 972, Ap	1085	69	3.9	542	4	US-09-949-016-6462	Sequence 6462, Ap
1013	69.5	3.9	456	4	US-09-438-185A-901	Sequence 901, App	1086	69	3.9	543	4	US-09-949-016-10085	Sequence 10085, A
1014	69.5	3.9	484	4	US-09-248-796A-15483	Sequence 15483, A	1087	69	3.9	561	4	US-09-198-452A-744	Sequence 744, App
1015	69.5	3.9	499	3	US-09-049-672A-1	Sequence 1, Appli	1088	69	3.9	584	4	US-09-911-909B-14	Sequence 14, Appli
1016	69.5	3.9	506	3	US-08-888-998-2	Sequence 2, Appli	1089	69	3.9	657	3	US-08-508-761B-2	Sequence 2, Appli
1017	69.5	3.9	506	3	US-09-362-633-2	Sequence 2, Appli	1090	69	3.9	673	3	US-08-196-387-8	Sequence 8, Appli
1018	69.5	3.9	506	4	US-09-877-476-28	Sequence 2, Appli	1091	69	3.9	673	4	US-08-841-835-8	Sequence 8, Appli
1019	69.5	3.9	506	4	US-09-877-476-28	Sequence 28, Appli	1092	69	3.9	688	4	US-09-071-035-464	Sequence 464, App
1020	69.5	3.9	506	4	US-09-877-476-36	Sequence 36, Appli	1093	69	3.9	712	4	US-09-949-016-10600	Sequence 10600, A
1021	69.5	3.9	512	4	US-09-248-796A-14219	Sequence 14219, A	1094	69	3.9	725	4	US-09-949-016-9976	Sequence 9976, Ap
1022	69.5	3.9	548	4	US-09-538-092-1058	Sequence 1058, Ap	1095	69	3.9	821	4	US-09-308-345A-48	Sequence 48, Appli
1023	69.5	3.9	555	4	US-09-328-352-5873	Sequence 5873, Ap	1096	69	3.9	851	4	US-09-543-681A-7277	Sequence 7277, Ap
1024	69.5	3.9	559	4	US-09-949-016-9137	Sequence 9137, Ap	1097	69	3.9	919	4	US-09-949-016-6954	Sequence 6954, Ap
1025	69.5	3.9	677	4	US-09-270-767-58094	Sequence 58094, A	1098	69	3.9	924	4	US-09-438-185A-704	Sequence 704, App
1026	69.5	3.9	697	4	US-09-486-072-3	Sequence 3, Appli	1099	69	3.9	949	3	US-09-196-387-10	Sequence 10, Appli
1027	69.5	3.9	742	4	US-09-494-297A-4	Sequence 4, Appli	1100	69	3.9	949	4	US-09-841-835-10	Sequence 10, Appli
1028	69.5	3.9	804	3	US-08-981-446B-3	Sequence 3, Appli	1101	69	3.9	1068	3	US-09-215-694-7	Sequence 7, Appli
1029	69.5	3.9	847	4	US-09-270-767-42783	Sequence 42783, A	1102	69	3.9	1327	3	US-09-196-387-2	Sequence 2, Appli
1030	69.5	3.9	898	4	US-09-949-016-10987	Sequence 10987, A	1103	69	3.9	1327	4	US-09-841-835-2	Sequence 2, Appli
1031	69.5	3.9	1260	3	US-08-506-296B-21	Sequence 21, Appli	1104	69	3.9	1327	4	US-09-972-115A-8	Sequence 8, Appli
1032	69.5	3.9	1722	4	US-09-194-612A-1	Sequence 1, Appli	1105	69	3.9	2032	4	US-09-071-035-458	Sequence 458, App
1033	69	3.9	108	2	US-08-378-939-30	Sequence 30, Appli	1106	69	3.9	2032	4	US-09-071-035-462	Sequence 462, App
1034	69	3.9	127	3	US-09-136-315-4	Sequence 4, Appli	1107	69	3.9	2032	4	US-09-071-035-466	Sequence 466, App
1035	69	3.9	127	4	US-09-767-888-4	Sequence 4, Appli	1108	69	3.9	2054	4	US-09-134-000C-6612	Sequence 6612, Ap
1036	69	3.9	156	3	US-08-821-994-42	Sequence 42, Appli	1109	69	3.9	3892	4	US-09-328-352-5503	Sequence 5503, Ap
1037	69	3.9	243	4	US-09-107-532A-6856	Sequence 6856, Ap	1110	69	3.9	4536	4	US-09-180-422B-27	Sequence 27, Appli
1038	69	3.9	269	2	US-08-727-311-3	Sequence 3, Appli	1111	69	3.9	4536	4	US-09-079-030-1	Sequence 1, Appli
1039	69	3.9	329	4	US-09-651-200-18	Sequence 18, Appli	1112	69	3.9	4563	4	US-09-108-006C-1	Sequence 1, Appli
1040	69	3.9	329	4	US-09-303-040-6	Sequence 6, Appli	1113	69	3.9	4563	4	US-09-538-092-842	Sequence 842, App
1041	69	3.9	329	4	US-09-710-279-414	Sequence 414, App	1114	68.5	3.9	105	2	US-08-820-754-22	Sequence 22, Appli
1042	69	3.9	331	3	US-09-134-001C-5258	Sequence 5258, Ap	1115	68.5	3.9	105	3	US-08-956-652-22	Sequence 22, Appli
1043	69	3.9	335	3	US-09-902-540-11829	Sequence 11829, A	1116	68.5	3.9	105	3	US-08-956-869-22	Sequence 22, Appli
1044	69	3.9	355	3	US-08-875-811-41	Sequence 41, Appli	1117	68.5	3.9	105	3	US-08-948-547-22	Sequence 22, Appli
1045	69	3.9	355	3	US-08-875-811-49	Sequence 49, Appli	1118	68.5	3.9	105	4	US-08-212-185-22	Sequence 22, Appli
1046	69	3.9	355	3	US-08-875-811-64	Sequence 64, Appli	1119	68.5	3.9	212	4	US-09-640-211A-796	Sequence 796, App
1047	69	3.9	357	4	US-09-949-016-9074	Sequence 9074, Ap	1120	68.5	3.9	217	4	US-09-291-299A-7	Sequence 7, Appli
1048	69	3.9	358	3	US-08-875-811-45	Sequence 45, Appli	1121	68.5	3.9	217	6	5189147-7	Sequence 7, Appli
1049	69	3.9	358	3	US-08-875-811-51	Sequence 51, Appli	1122	68.5	3.9	217	6	5189147-7	Patent No. 5189147





```
1415 66.5 3.8 422 3 US-08-477-346-55 Sequence 55, Appl Sequence 9, Appli
1416 66.5 3.8 422 3 US-08-473-089-53 Sequence 55, Appl Sequence 8, Appli
1417 66.5 3.8 422 3 US-08-473-089-55 Sequence 55, Appl Sequence 9, Appli
1418 66.5 3.8 422 4 US-08-487-072A-53 Sequence 55, Appl Sequence 40, Appli
1419 66.5 3.8 422 4 US-08-487-072A-55 Sequence 55, Appl Sequence 8, Appli
1420 66.5 3.8 422 4 US-08-538-092-48 Sequence 48, Appl Sequence 9, Appli
1421 66.5 3.8 432 3 US-08-477-460B-2 Sequence 2, Appli Sequence 8, Appli
1422 66.5 3.8 432 3 US-08-379-516-2 Sequence 2, Appli Sequence 9, Appli
1423 66.5 3.8 432 3 US-09-329-916-2 Sequence 2, Appli Sequence 34508, A
1424 66.5 3.8 432 3 US-08-485-372A-2 Sequence 2, Appli Sequence 49725, A
1425 66.5 3.8 432 4 US-09-409-006A-2 Sequence 2, Appli Sequence 7324, Ap
1426 66.5 3.8 432 4 US-08-484-681-2 Sequence 2, Appli Sequence 166, App
1427 66.5 3.8 432 4 US-09-766-995-2 Sequence 2, Appli Sequence 44, Appli
1428 66.5 3.8 432 5 PCT-US93-07422-2 Sequence 4, Appli
1429 66.5 3.8 458 3 US-08-466-368-4 Sequence 4, Appli
1430 66.5 3.8 458 3 US-09-517-605-3 Sequence 3, Appli
1431 66.5 3.8 461 1 US-08-194-338-4 Sequence 4, Appli
1432 66.5 3.8 463 4 US-09-248-796A-18855 Sequence 18855, A
1433 66.5 3.8 499 4 US-09-902-540-15512 Sequence 15512, A
1434 66.5 3.8 581 2 US-08-724-39A-2 Sequence 2, Appli
1435 66.5 3.8 610 3 US-09-019-160-4 Sequence 4, Appli
1436 66.5 3.8 630 4 US-09-949-016-6828 Sequence 6828, Ap
1437 66.5 3.8 677 3 US-09-019-160-3 Sequence 3, Appli
1438 66.5 3.8 682 4 US-09-937-521-14 Sequence 14, Appli
1439 66.5 3.8 708 3 US-09-019-160-5 Sequence 5, Appli
1440 66.5 3.8 756 4 US-09-937-521-13 Sequence 13, Appli
1441 66.5 3.8 819 4 US-09-949-016-11044 Sequence 11044, A
1442 66.5 3.8 893 3 US-09-019-160-6 Sequence 6, Appli
1443 66.5 3.8 893 3 US-09-019-160-7 Sequence 7, Appli
1444 66.5 3.8 893 3 US-09-019-160-8 Sequence 8, Appli
1445 66.5 3.8 893 3 US-09-019-160-9 Sequence 9, Appli
1446 66.5 3.8 896 2 US-08-640-389A-10 Sequence 10, Appli
1447 66.5 3.8 906 2 US-08-640-389A-9 Sequence 9, Appli
1448 66.5 3.8 958 2 US-08-640-389A-8 Sequence 8, Appli
1449 66.5 3.8 998 4 US-10-101-464A-931 Sequence 931, App
1450 66.5 3.8 1041 4 US-10-144-198-14 Sequence 14, Appli
1451 66.5 3.8 1165 2 US-08-640-389A-11 Sequence 11, Appli
1452 66.5 3.8 1296 4 US-08-857-636-60 Sequence 60, Appli
1453 66.5 3.8 1447 2 US-08-540-406-19 Sequence 19, Appli
1454 66.5 3.8 1447 3 US-08-656-055-19 Sequence 19, Appli
1455 66.5 3.8 1447 3 US-08-954-668-19 Sequence 19, Appli
1456 66.5 3.8 1447 3 US-09-041-886-25 Sequence 25, Appli
1457 66.5 3.8 1447 3 US-09-268-140-5 Sequence 5, Appli
1458 66.5 3.8 1447 4 US-08-918-658-19 Sequence 19, Appli
1459 66.5 3.8 1447 4 US-09-724-631-19 Sequence 19, Appli
1460 66.5 3.8 1447 4 US-08-954-701A-19 Sequence 19, Appli
1461 66.5 3.8 1447 5 PCT-US94-05277-2 Sequence 2, Appli
1462 66.5 3.8 1447 5 US-08-472-788A-27 Sequence 27, Appli
1463 66 3.7 107 1 US-08-107-669D-27 Sequence 27, Appli
1464 66 3.7 107 2 US-08-477-531B-27 Sequence 27, Appli
1465 66 3.7 107 2 US-08-477-531B-27 Sequence 27, Appli
1466 66 3.7 116 3 US-08-082-842A-27 Sequence 27, Appli
1467 66 3.7 116 3 US-09-184-658-48 Sequence 48, Appli
1468 66 3.7 116 4 US-09-504-262D-48 Sequence 48, Appli
1469 66 3.7 128 2 US-08-379-057-12 Sequence 12, Appli
1470 66 3.7 151 4 US-09-248-796A-24027 Sequence 24027, A
1471 66 3.7 174 2 US-08-459-135A-10 Sequence 10, Appli
1472 66 3.7 174 3 US-08-495-559-10 Sequence 10, Appli
1473 66 3.7 175 4 US-09-270-767-60065 Sequence 60065, A
1474 66 3.7 176 3 US-08-495-559-6 Sequence 6, Appli
1475 66 3.7 181 2 US-08-459-135A-6 Sequence 6, Appli
1476 66 3.7 229 4 US-09-134-000C-3584 Sequence 3584, Ap
1477 66 3.7 231 3 US-08-974-380-2 Sequence 2, Appli
1478 66 3.7 231 4 US-09-546-977A-2 Sequence 2, Appli
1479 66 3.7 231 4 US-09-654-466-2 Sequence 2, Appli
1480 66 3.7 269 3 US-09-070-408-132 Sequence 132, App
1481 66 3.7 286 4 US-09-270-767-44618 Sequence 44618, A
1482 66 3.7 289 3 US-09-184-658-63 Sequence 63, Appli
1483 66 3.7 289 4 US-09-504-262D-63 Sequence 63, Appli
1484 66 3.7 314 6 5434340-7 Patent No. 5434340
1485 66 3.7 314 6 5434340-7 Patent No. 5434340
1486 66 3.7 340 2 US-08-633-148-2 Sequence 2, Appli
1487 66 3.7 365 3 US-09-195-666A-8 Sequence 8, Appli
```

```
1488 66 3.7 365 3 US-09-195-666A-9 Sequence 9, Appli
1489 66 3.7 365 3 US-09-635-705-8 Sequence 8, Appli
1490 66 3.7 365 3 US-09-635-705-9 Sequence 9, Appli
1491 66 3.7 365 4 US-09-336-536-40 Sequence 40, Appli
1492 66 3.7 365 4 US-09-634-858A-8 Sequence 8, Appli
1493 66 3.7 365 4 US-09-634-858A-9 Sequence 9, Appli
1494 66 3.7 365 4 US-08-869-927C-8 Sequence 8, Appli
1495 66 3.7 365 4 US-08-869-927C-9 Sequence 9, Appli
1496 66 3.7 368 4 US-09-270-767-34508 Sequence 34508, A
1497 66 3.7 368 4 US-09-270-767-49725 Sequence 49725, A
1498 66 3.7 368 4 US-09-489-039A-7324 Sequence 7324, Ap
1499 66 3.7 374 4 US-09-489-847-166 Sequence 166, App
1500 66 3.7 376 4 US-09-721-870-44 Sequence 44, Appli
```

## ALIGNMENTS

## RESULT 1

```
US-09-513-999C-4472
; Sequence 4472, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A. J.Y.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4472
; LENGTH: 97
```

```
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: -22...-1
;; OTHER INFORMATION: score 5.9
;; OTHER INFORMATION: seq LIYILWQLTGSAA/SG
US-09-513-999C-4472
```

Query Match 28.1%; Score 498; DB 4; Length 97;

Best Local Similarity 100.0%; Pred. No. 6.9e-46; Mismatches 0; Indels 0; Gaps 0;

Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTIYILWQLTGSAAAGPVKELVSGVAVTFPLKSKVKQVDSIVTFTNTPL 60

Db 1 MAGSPCTCLTIYILWQLTGSAAAGPVKELVSGVAVTFPLKSKVKQVDSIVTFTNTPL 60

QY 61 VTIOEGGTIIVTQNRNRERVDPPDGYSLSKLK 97

Db 61 VTIOEGGTIIVTQNRNRERVDPPDGYSLSKLK 97

## RESULT 2

```
US-09-949-016-6428
; Sequence 6428, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
```

```
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6428
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6428

Query Match      20.5%; Score 362.5; DB 4; Length 328;
Best Local Similarity 31.5%; Pred. No. 2.3e-30;
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;

QY 14 LWQL-----TGSAAAGPVKELV--GSGVGAATPLK-SKVKQVDSIVYVNTTTLVLTIIQ 64
Db 6 LLLLLLQCTWPEAAGKQSEIPTVNGILGESVTFPNTQEPQVKIIAWTSKTSVAYVTP 65

QY 65 PEGGT---IIVTONRRRVRDPDGGYSLKLSKLNKNDGIIYVGIYSSSLQQPSTORYV 121
Db 66 GDSFAPVTVTHRYNRYERHALGPNYNLVISDLRWDAGDYKADINTQADPYTTTKYN 125

QY 122 LHVYEHLSKPKVTGMLQNKGTCTVNTTCMEHGEEDVIYTWKALQQAANESHGSLP 181
Db 126 LQIVRRGLGPKITQSLMASVNSTCVNTLTCSVEKEKNVTYNWSPGSE-----EGNVLQ 179

QY 182 ISWRGSGDMTFICVARNPVSRNFSSPILARKICEGAADDDPS-----SMVLLCLLAVP 235
Db 180 IQPTEDQLYTTCTAQPVSNN-SDSISARQLCADIANGFRTHHTGLLSVLAMFLLVL 238

QY 236 LLLSLVFLGLFLWFLKRRQREYIEBKRVDCITPNICPHSGENTSYDIPHTNRTIL 295
Db 239 ILSSVFLRLF-----KRDQAASKTYITYIMASRNTQP--AESRIYDELQSKVLPS 290

QY 296 KEDPANTVYSTVEIPKQENPHSLTMDPTPLRFAYENVI 335
Db 291 KEEPVNTVYSEQFADKMGKASTQDSKP--PGTSSYEIVI 328

RESULT 3
US-09-149-476-483
; Sequence 483, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002PI
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,502
```

EARLIER APPLICATION NUMBER: 60/056,878  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,662  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,872  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,882  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,637  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,903  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,888  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,879  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,880  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,894  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,911  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,636  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,874  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,910  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,864  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,599  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,588  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,585  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,586  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,590  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,594  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,589  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,593  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881

EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 20.5%; Score 362.5; DB 4; Length 329;  
Best Local Similarity 31.5%; Pred. No. 2.3e-30; Indels 35; Gaps 10;  
Matches 107; Conservative 55; Mismatches 143

QY 14 LWQL-----TGSAAAGPVKVELY---GSVGGAVTFPLK-SKVQVDSIVVTFNTPLVLTQ 64  
DB 6 LWILLCLLTWPEAGKSEIFTVNGILGESVTFPNIOEPQVKIANTSKTSVAVYVP 65  
QY 65 PEGGT---IIVTONRRERVPDPDGGYSLKLSKLNKNSGIYVYGVYSSLOQPSQYEV 121  
DB 66 GDSCTAPVTVTHRYNRYERHALGPNYNLVISDLRMEADAGYKADINTQADPYTTTKRYN 125  
QY 122 LHVEHLSKPKVTMGLOSNGKCTVNTLTCMHEGEEDVIYTWKALGOANESHNGSIPL 181  
DB 126 LQIYRLGKPKITQSLMASVNSTVNTLTCSVEKEKNVTYNWSPLGE-----EGNVLQ 179  
QY 182 ISWRMGESDMTFCVARNPVSFNFSPIARLKLCEGAADDPDS-----SMVLLCLLLVP 235  
DB 180 IFQTPEDQELTYCTAQNPNVNN-SDSISARQLCADIANGFTHHTGLLSVLAMPFLVLL 238  
QY 236 LLLSLFVLGLFWFLKRRQEEYIEKKRVDCRETPNICPHSGENTYDITPHNTNRTL 295  
DB 239 ILSSVFLFLF-----KRRQDAASKKTYTYVIMASRNTQP--ABSRIYDEILQSKVLPS 290  
QY 296 KEDPANTYVSTVEIPKMNPHSLTMDTPRLPAYENVI 335  
DB 291 KEEPVNTYVSEVQFADRMKASTQDSKP--PGTSSYEIVI 328

RESULT 4  
US-09-949-016-7327  
Sequence 7327, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7327

```
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7327

Query Match      20.5%; Score 362.5; DB 4; Length 332;
Best Local Similarity 31.5%; Pred. No. 2.3e-30;
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;

QY 14 LWQL-----TGAAGPQVKELV---GSGGAVTFPLK-SKVQVDSIVMTNTPLVTIQ 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 10 LMIILLCLQTWEPAAGKDEIFVTNGILGESVTFPNIQEPQVQKIIAINTSKTSVAYTP 69
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 65 PEGGT---IIVQNRRERVDPPDGGYSLKLSLKKNDSDGIYVYSSSQQPSTORYV 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 70 GDSAPVTVVTHRYERIHAGLPNVLVSDLAMEDAGDYKADINTQADPYTTTKRYN 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 122 LHVYHLSKPKVTMGLOSNKNGTCVNTLTCMHEGEEDVIYTWKALGOANESHNGSLP 181
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 LQIYRRLGPKKITQSLMASVNSTCNVTLTCSVEKEKNVTYNWSPFGE-----EGNVLQ 183
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 182 ISRWGESDMTFCVARNPVSNSFSPILARKLCGAADDDPS-----SMVLLCLLLVP 235
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 IFQTEDQELTYCTAQPVSNN-SDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVL 242
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 236 LLLSLFVLGLFLWFLKRRQEEYIEBKRRVDICRETPNICPHSGENTBYDTIPNRTIL 295
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 243 ILLSVFLFLF-----KRRQDAASKKTIYTIMASRNTQP--AESRIYDEILQSKVLPS 294
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 296 KEDPANTYVSTVEIPKMNPHSLTMDPTPLFAYENVI 335
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 295 KEEPVNTYSEVQFADKMGKASTQSKP--PGTSSYEIVI 332
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
US-08-348-792-10
; Sequence 10, Application US/08348792
; Patent No. 5576423
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,792
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-348-792-10

Query Match      10.5%; Score 186; DB 1; Length 343;
Best Local Similarity 24.3%; Pred. No. 3e-11;
Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;

QY 8 LTLIYIWLQLTGAASG---PVKELVSGVGAVTFPL-----KSKVKQVDSIVWTFN 56
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 12 LLFLSLAFELSYGTGGVMDCPV--ILQKLGQDTWLPILTNEHQINKSVKSVRIILV-TWA 68
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 57 TTPLVTIQPEGGTIIVTONRRERVD-----PD---GGY-----SLKLSLKKND 99
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 69 TSP-----GSKSNKIVSFDLSKSGSPDHLDEGYHFQSKNLSLKILGNRRS 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 100 SGIYVVGIYSS-SLQOPSTQEVVLHVYHLSKP--KVTMGLQSNKNGTCVNTLTCMHBG 156
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 116 EGVLDVSEENVSVQOFCQ---LKYEQVSPPEIKVINKTQENENGTCSSLLACTVKKG 172
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 157 BEDVIYTWK-----ALGOANESHNGSILPISRWGESDMTFCVARNPV---SRNFSP 208
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 DH-VTYSWSDRAGTHLLSRANSH---LLHITLSNQHQDSIYNCVTASNVPSSISRTFN-- 226
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 209 ILARKLCGAADDDPSMWLLCLLLVPLLLSLFVLGLFLWFLKRRQEEYIE---EKRV 265
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 227 -LSSQACKQESSSSSPMMQYTLVPLGVIIIFILVFTAILMMKQKQKSNHCQPPVVEKSL 285
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 266 DICRETPNICPHSGENTBYDTIPNRTILKEDPANTYV--STVEIPKKMENP-----HS 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 286 TIYAQVQKSGPQ--EKKLHD-----ALTDODPCTTIYVAATBPAPESVQEPNPTTVYA 336
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 319 LLTMPDT 325
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 337 SVTLPE 343
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```



```
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-738-10

Query Match      10.5%; Score 186; DB 2; Length 343;
Best Local Similarity 24.3%; Pred. No. 3e-11;
Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;

QY 8 LTLIYLWQLTGSASG-----PVKELVSGVGAVTFPL-----KSKVKQVDSIVWTFN 56
DB 12 LLFLSLAFELSYGTGGVWDCPV--ILQKLGQDTWPLPLTNEHQINKSVNKSVRILV-TWA 68

QY 57 TTPPLVTIQPEGGTIIVTQNRNRVDF-----PD---GGY-----SLKSLKLNKD 99
DB 69 TSP-----GSKSNKKIVSFDLSKGSYPDLHLEDGYHFQSKNLSLKILGNRRS 115

QY 100 SGIVYVGIYSS-SLOQPSTQEVVLHVYEHLSKP--KVTWGLQSNKNGTCVTNLTCCMEHG 156
DB 116 EGWILSVSENVSVQOFCQ---LKYEQVSPPEIKVLNKTQENENGTCSLLLACTVKKG 172

QY 157 EEDVITYTWK-----ALGOANESHGSIPLPSRWGESDMTFICVARNPV---SRNFSP 208
DB 173 DH-VTYSWSDRAGTHLLSRANSH---LLHITLSNQHQDSIYNCTASNPVSSISRTFN-- 226

QY 209 ILARKLCEGAADDPSSMVLCLLAVPLLLSLFVLGLFWFLKRRQBEYIE---EKRRV 265
DB 227 -LSSQACKQESSSESPWQYTLVPLGVVFIILVFTALIMMKROCKSNHCOPPVEEKSL 285

QY 266 DICRETNPICHSAGENTYDTPHTNRTILKEDPANTVY--STVEIPKQENP-----HS 318
DB 286 TIYAQVQKSGPQ--EKKLHD-----ALTDQDPTTIYVAATEPAPESVQEPNPTTYA 336

QY 319 LLTMPDT 325
DB 337 SVTLPE 343
```

## RESULT 7

```
US-09-199-955-10
Sequence 10, Application US/09199955
Patent No. 6372899
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,955
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,473
```

```
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-199-955-10

Query Match      10.5%; Score 186; DB 3; Length 343;
Best Local Similarity 24.3%; Pred. No. 3e-11;
Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;

QY 8 LTLIYLWQLTGSASG-----PVKELVSGVGAVTFPL-----KSKVKQVDSIVWTFN 56
DB 12 LLFLSLAFELSYGTGGVWDCPV--ILQKLGQDTWPLPLTNEHQINKSVNKSVRILV-TWA 68

QY 57 TTPPLVTIQPEGGTIIVTQNRNRVDF-----PD---GGY-----SLKSLKLNKD 99
DB 69 TSP-----GSKSNKKIVSFDLSKGSYPDLHLEDGYHFQSKNLSLKILGNRRS 115

QY 100 SGIVYVGIYSS-SLOQPSTQEVVLHVYEHLSKP--KVTWGLQSNKNGTCVTNLTCCMEHG 156
DB 116 EGWILSVSENVSVQOFCQ---LKYEQVSPPEIKVLNKTQENENGTCSLLLACTVKKG 172

QY 157 EEDVITYTWK-----ALGOANESHGSIPLPSRWGESDMTFICVARNPV---SRNFSP 208
DB 173 DH-VTYSWSDRAGTHLLSRANSH---LLHITLSNQHQDSIYNCTASNPVSSISRTFN-- 226

QY 209 ILARKLCEGAADDPSSMVLCLLAVPLLLSLFVLGLFWFLKRRQBEYIE---EKRRV 265
DB 227 -LSSQACKQESSSESPWQYTLVPLGVVFIILVFTALIMMKROCKSNHCOPPVEEKSL 285

QY 266 DICRETNPICHSAGENTYDTPHTNRTILKEDPANTVY--STVEIPKQENP-----HS 318
DB 286 TIYAQVQKSGPQ--EKKLHD-----ALTDQDPTTIYVAATEPAPESVQEPNPTTYA 336

QY 319 LLTMPDT 325
DB 337 SVTLPE 343
```

## RESULT 8

```
US-08-880-875-10
Sequence 10, Application US/08880875
Patent No. 6399065
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/880,875  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/481,777  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/348,792  
FILING DATE: 02-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0436K  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 343 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-880-875-10

Query Match 10.5%; Score 186; DB 3; Length 343;  
Best Local Similarity 24.3%; Pred. No. 3e-11;  
Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;  
QY 8 LTIYILMQLTGSAAAG-----PVKELVSGVGAVTFPL-----KSKVKQVDSIVWTFN 56  
DB 12 LLFLSLAFELSYGTGGVMDCEV--ILQKLGQDTWLPNTNEHQINKSVNKSVRILV-TWA 68  
QY 57 TPLVTIQPEGTTIVTQNRNRVDF-----PD-----GGY-----SLKSLKKND 99  
DB 69 TSP-----GSKSNKKIYSPDLKSGSYPDHLEDGYHFQSKNLSKILGNRRS 115  
QY 100 SGIVYVGYSS-SLOQPSTQEVVLHVYHLSP--KVTMGLQSNKNGTCVNTLTCMEHG 156  
DB 116 EGWILVSVENSVQOFCKQ---LKLYEQVSPPEIKVLNKTOENENGCSLLACTVKG 172  
QY 157 EEDVITYTWK-----ALGOAANESHGSIPIPSWRWGESDMPFICVARNPV---SRNFSP 208  
DB 173 DH-VIYSDSEAGTHLLSPNRSH---LLHITLSNQHODSIYNCATSNPVSSISRTFN-- 226  
QY 209 ILARKLCGAADDPSSVLLCLLVPDLLSLFVLGLFLWFLKRRQEEYIE---EKRV 265  
DB 227 -LSSQACKQESSSESPWQYTLVPLGVVIFILVFTAILMMKROGKNHCQPPVEEKS 285  
QY 266 DICRETPNICPSGENTYDTPHTNRTILKEDPANTVY--STVEIPKKNP-----HS 318  
DB 286 TIYAVQVSGGP--BKULHD-----ALTDQDCTTIYVAATEPAPESVQEPNPTTYA 336  
QY 319 LITMPDT 325  
DB 337 SVTLPE 343

RESULT 9  
US-08-348-792-2  
Sequence 2, Application US/08348792  
Patent No. 5576423  
GENERAL INFORMATION:  
APPLICANT: Aversa, Gregorio  
APPLICANT: Chang, Chia-Chun J.  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: de Vries, Jan E.  
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSER: DNAX Research Institute

STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/348,792  
FILING DATE: 02-DEC-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0436  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 335 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-348-792-2

Query Match 10.3%; Score 182.5; DB 1; Length 335;  
Best Local Similarity 22.5%; Pred. No. 6.8e-11;  
Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;  
QY 8 LTIYILM-QLTGSAAGP-----VKELVSGVGAVTFPL-----KSKVKQVDSIVWT 54  
DB 7 LSLTFVLFLSLAFAGSYGTGGRMNCPKILQKLGSKVLLPLTYERINKSMKSHIVTM 66  
QY 55 FNT-----TPLVTIQP--EGGTIIIVTQNRNRVDFPDGGYSLKSLKNDSGIYVGI 107  
DB 67 AKSLSENSVENKIVSLDPSEAG---PPRYLGDYKVFYLENLTGLIRESKKEDEGWYMTL 122  
QY 108 YSS-SLOQPSTQEVVLHVYHLSPKVTMGLQSNKNGTCVNTLTCMEHGSDVITYW-- 164  
DB 123 EKNVSVORFCLQ---LRLYEQVSTPEIKVLNKTOENGTCTILGCTVEKGDH-VAYSWE 178  
QY 165 KALGOAANESHGSIPIPSWRWGESDMPFICVARNPVSRNFS--SPILARKLCEGAADP 222  
DB 179 KAGTHPLNPANSHLLSLTLGPQHADNIYICTVSNPISNNSQTFSP-----WPCRTDP 232  
QY 223 DSSM-----VLICLLLVPLLISLFLVLGLFLWFLKRRQEEYIE---EKRV 268  
DB 233 SETXPAVYAGLGGVIMLIMVILQ-----LRRGKTNHYQTVEKSLIY 281  
QY 269 RETPNICPSGENTYDTPHTNRTILKEDPANTVY--STVEIPKKNP-----LT 321  
DB 282 AQVQKPGP---LQKKLDSFP-----AQDPCTTIYVAATEPVPESVQETNSITVYASVT 331  
QY 322 MPDT 325  
DB 332 LPES 335

RESULT 10  
US-08-462-738-2  
Sequence 2, Application US/08462738  
Patent No. 5977303  
GENERAL INFORMATION:  
APPLICANT: Aversa, Gregorio  
APPLICANT: Chang, Chia-Chun J.  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: de Vries, Jan E.  
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL  
SURFACE ANTIGENS; PROTEINS AND ANTIBODIES



Db 332 LPES 335

RESULT 12

US-08-880-875-2

; Sequence 2, Application US/08880875

; Patent No. 6399065

; GENERAL INFORMATION:

; APPLICANT: Aversa, Gregorio

; APPLICANT: Chang, Chia-Chun J.

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Ge Vries, Jan E.

; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL

; SURFACE ANTIGENS; PROTEINS AND ANTIBODIES

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute

; STREET: 901 California Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/880,875

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/481,777

; FILING DATE: 07-JUN-1995

; APPLICATION NUMBER: US 08/348,792

; FILING DATE: 02-DEC-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0436K

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-852-9196

; TELEFAX: 415-496-1200

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 335 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-880-875-2

Query Match 10.3%; Score 182.5; DB 3; Length 335;

Best Local Similarity 22.5%; Pred. No. 6.8e-11;

Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;

QY 8 LTLVIILW-QLTGSAAAGP-----VKELVSGVGGAVTFPL-----KSKVKQVDSIVMT 54

Db 7 LSLTFVLFLSLAFGASYGTGGRMNCPKILRQLGSKVLLPLTYERINKSMNKSIIHVMT 66

QY 55 FNT-----TPLVTIOP-EGGTIIIVTONRNRERVDPPDGGYSLKLSKLKNDSGIYYVGI 107

Db 67 AKSLSENSVENKIVSLDPSEAG----PPRYLGDYKVFYLENLTLGIRSRKDEGWYMTL 122

QY 108 YSS-SLOQPSTQEVYLVHYEHLKPKVTMGLOSNGKTCVTNLTCCMEHGEEDVIYTW-- 164

Db 123 EKNVSQVORFCIQ---LRLYEQVSTPEIKVLNKTQENGCTTLILGCTVEKGDH-VAYSWS 178

QY 165 KALQQAANESHNGSILPISWRGSDMTFICVARNPVSRNFS--SPILARKLCEGAADDP 222

Db 179 KAGTHPLPANSHLLSLTLGPHQADNIYICTVSNPISNNSTQTFP-----WPCRTDP 232

QY 223 DSSM-----VLICLLLVPLLLSLFVLGLFWFLKRRQBEYIE---EKRRVDIC 268

Db 233 SETKPWAVYAGLGGVIMILIMVILQ-----LRRGKTNHYQTTVEKKSLLTY 281

QY 269 RETPNI CPHSGENTYDTIPIHTNRILKEDPANTVY--STVEIPKPMENPHSL-----LT 321

Db 282 AQVKPGP---LQKKLDSFP-----AQDPCTTIYVAATEPVPESVQETNSITVYASVT 331

QY 322 MPDT 325

Db 332 LPES 335

RESULT 13

US-09-369-248A-3

; Sequence 3, Application US/09369248A

; Patent No. 6620912

; GENERAL INFORMATION:

; APPLICANT: Young, Steven M.

; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Dendritic Enriched Secreted Lymphocyte Activation

; MOLECULE

; FILE REFERENCE: PF448P1

; CURRENT APPLICATION NUMBER: US/09/369,248A

; CURRENT FILING DATE: 1999-08-05

; PRIOR APPLICATION NUMBER: 60/073,962

; PRIOR FILING DATE: 1998-02-06

; PRIOR APPLICATION NUMBER: 60/078,572

; PRIOR FILING DATE: 1998-03-19

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 3

; LENGTH: 335

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-369-248A-3

Query Match 10.3%; Score 182.5; DB 4; Length 335;

Best Local Similarity 22.5%; Pred. No. 6.8e-11;

Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;

QY 8 LTLVIILW-QLTGSAAAGP-----VKELVSGVGGAVTFPL-----KSKVKQVDSIVMT 54

Db 7 LSLTFVLFLSLAFGASYGTGGRMNCPKILRQLGSKVLLPLTYERINKSMNKSIIHVMT 66

QY 55 FNT-----TPLVTIOP-EGGTIIIVTONRNRERVDPPDGGYSLKLSKLKNDSGIYYVGI 107

Db 67 AKSLSENSVENKIVSLDPSEAG----PPRYLGDYKVFYLENLTLGIRSRKDEGWYMTL 122

QY 108 YSS-SLOQPSTQEVYLVHYEHLKPKVTMGLOSNGKTCVTNLTCCMEHGEEDVIYTW-- 164

Db 123 EKNVSQVORFCIQ---LRLYEQVSTPEIKVLNKTQENGCTTLILGCTVEKGDH-VAYSWS 178

QY 165 KALQQAANESHNGSILPISWRGSDMTFICVARNPVSRNFS--SPILARKLCEGAADDP 222

Db 179 KAGTHPLPANSHLLSLTLGPHQADNIYICTVSNPISNNSTQTFP-----WPCRTDP 232

QY 223 DSSM-----VLICLLLVPLLLSLFVLGLFWFLKRRQBEYIE---EKRRVDIC 268

Db 233 SETKPWAVYAGLGGVIMILIMVILQ-----LRRGKTNHYQTTVEKKSLLTY 281

QY 269 RETPNI CPHSGENTYDTIPIHTNRILKEDPANTVY--STVEIPKPMENPHSL-----LT 321

Db 282 AQVKPGP---LQKKLDSFP-----AQDPCTTIYVAATEPVPESVQETNSITVYASVT 331

QY 322 MPDT 325

Db 332 LPES 335

RESULT 14

US-08-348-792-8

; Sequence 8, Application US/08348792

; Patent No. 5576423

; GENERAL INFORMATION:

APPLICANT: Aversa, Gregorio  
APPLICANT: Chang, Chia-Chun J.  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: de Vries, Jan E.  
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL  
SURFACE ANTIGENS; PROTEINS AND ANTIBODIES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/348,792  
FILING DATE: 02-DEC-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0436  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 307 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-348-792-8

Query Match 10.2%; Score 180; DB 1; Length 307;  
Best Local Similarity 22.6%; Pred. No. 1.1e-10;  
Matches 76; Conservative 67; Mismatches 120; Indels 74; Gaps 17;  
QY 28 ELVSGVGAVTFPL-----KSKVKQVDSIVWTFNT-----TPLVTIQP-BGGTIIVTQ 74  
DB 6 KILRLGSKVLLPLTYERINKSMNKSIIHVVTMAKSLNSVENKIVSLDPSAG---PP 61  
QY 75 NNRERVDPPDGGYSLKSLKKNDSGIYVGIYS-SLQOPSTQYVHLVHVEHLSKPKV 133  
DB 62 RYLGRYKYLENLTLGIRSRKEDEGWYLTLEKNVSVQRFCLQ---LRLYEQVSTPEI 118  
QY 134 TMGLQSNKNGTCVTNLTCCMEHGEDVITYW--KALGOANESHNGSILPISWRNGESDM 191  
DB 119 KVLNKTQENGCTTLIGCTVEKGDH-VAYSWEKAGTHPLNPANSHLLSLTLGPOHADN 177  
QY 192 TFCIVARNPVSRNFS--SPILARKLCEGAADPDSSM-----VLLCLLVLPLLL 238  
DB 178 IYICTVSNPISNSQTFSP-----WPGCRTPDSEKTPWVAVAGLLGGVIMLIMVILQ 231  
QY 239 SLFVLGLFLWFLKRRQBEYIE---EKRVDCRETNICPHSGENTYDTPHNTIL 295  
DB 232 -----LRRRGKTNHYQTIVVEKSLTIYAQVQKPGP---LQKLDSPF----- 270  
QY 296 KEDPANTVY--STVEIPKKMENPHSL-----LTMPDT 325  
DB 271 AQDPCTTIYVAATEPVPSVQETNSITVYASVTLPE 307

## RESULT 15

US-08-462-738-8  
Sequence 8, Application US/08462738  
Patent No. 5977303  
GENERAL INFORMATION:  
APPLICANT: Aversa, Gregorio

APPLICANT: Chang, Chia-Chun J.  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: de Vries, Jan E.  
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL  
SURFACE ANTIGENS; PROTEINS AND ANTIBODIES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,738  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/348,792  
FILING DATE: 02-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0436GB  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 307 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-462-738-8

Query Match 10.2%; Score 180; DB 2; Length 307;  
Best Local Similarity 22.6%; Pred. No. 1.1e-10;  
Matches 76; Conservative 67; Mismatches 120; Indels 74; Gaps 17;  
QY 28 ELVSGVGAVTFPL-----KSKVKQVDSIVWTFNT-----TPLVTIQP-BGGTIIVTQ 74  
DB 6 KILRLGSKVLLPLTYERINKSMNKSIIHVVTMAKSLNSVENKIVSLDPSAG---PP 61  
QY 75 NNRERVDPPDGGYSLKSLKKNDSGIYVGIYS-SLQOPSTQYVHLVHVEHLSKPKV 133  
DB 62 RYLGRYKYLENLTLGIRSRKEDEGWYLTLEKNVSVQRFCLQ---LRLYEQVSTPEI 118  
QY 134 TMGLQSNKNGTCVTNLTCCMEHGEDVITYW--KALGOANESHNGSILPISWRNGESDM 191  
DB 119 KVLNKTQENGCTTLIGCTVEKGDH-VAYSWEKAGTHPLNPANSHLLSLTLGPOHADN 177  
QY 192 TFCIVARNPVSRNFS--SPILARKLCEGAADPDSSM-----VLLCLLVLPLLL 238  
DB 178 IYICTVSNPISNSQTFSP-----WPGCRTPDSEKTPWVAVAGLLGGVIMLIMVILQ 231  
QY 239 SLFVLGLFLWFLKRRQBEYIE---EKRVDCRETNICPHSGENTYDTPHNTIL 295  
DB 232 -----LRRRGKTNHYQTIVVEKSLTIYAQVQKPGP---LQKLDSPF----- 270  
QY 296 KEDPANTVY--STVEIPKKMENPHSL-----LTMPDT 325  
DB 271 AQDPCTTIYVAATEPVPSVQETNSITVYASVTLPE 307

Search completed: July 14, 2005, 13:29:00  
Job time : 40 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 14, 2005, 13:26:49 ; Search time 64 Seconds  
(without alignment)  
2022.207 Million cell updates/sec

Perfect score: 1772  
Sequence: 1 MAGSPCTCLTIVILWQLTGS.....PHSLLTMDPTRLPAYENVI 335

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1726220 seqs, 386332138 residues

Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 1500 summaries

Database : Published Applications AA:\*

1: /cgm2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgm2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgm2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*  
4: /cgm2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgm2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgm2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgm2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgm2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgm2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgm2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgm2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgm2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgm2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgm2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgm2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgm2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgm2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep.\*  
18: /cgm2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
19: /cgm2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*  
20: /cgm2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgm2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgm2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1772	100.0	335 9	US-09-732-524-2
8	1772	100.0	335 9	US-09-745-605-4
29	1772	100.0	335 10	US-09-997-428-253
540	1772	100.0	335 14	US-10-021-741A-2
565	1772	100.0	335 14	US-10-174-587-192
629	1772	100.0	335 14	US-10-063-742-46
739	1772	100.0	335 15	US-10-262-839-110
745	1772	100.0	335 17	US-10-842-011-2
746	1772	100.0	335 17	US-10-972-317-46
747	1769	99.8	335 14	US-10-104-943-5
748	1769	99.8	335 14	US-10-436-523-60
749	1769	99.8	335 16	US-10-408-765A-1405

750	1755.5	99.1	348	15	US-10-262-839-112	Sequence 112, App
751	1853	93.3	312	9	US-09-732-524-4	Sequence 4, Appli
752	582	32.8	110	9	US-09-984-245-125	Sequence 125, App
753	582	32.8	110	10	US-09-966-262-125	Sequence 125, App
754	582	32.8	110	10	US-09-983-966-125	Sequence 125, App
755	582	32.8	110	14	US-10-059-395-125	Sequence 125, App
756	582	32.8	110	14	US-10-143-090-125	Sequence 125, App
757	582	32.8	110	17	US-10-960-251-125	Sequence 125, App
758	471	28.6	91	9	US-09-864-761-41706	Sequence 41706, A
759	362.5	20.5	328	14	US-10-104-943-4	Sequence 4, Appli
760	362.5	20.5	328	14	US-10-436-523-30	Sequence 30, Appli
761	362.5	20.5	328	16	US-10-723-860-1886	Sequence 1886, Ap
762	362.5	20.5	328	17	US-10-684-206-8	Sequence 8, Appli
763	362.5	20.5	329	10	US-09-809-391-483	Sequence 483, App
764	362.5	20.5	329	10	US-09-882-171-483	Sequence 483, App
765	362.5	20.5	329	15	US-10-164-861-483	Sequence 483, App
766	345.5	19.5	301	17	US-10-311-829-11	Sequence 11, Appli
767	343	19.4	629	10	US-09-860-836B-9	Sequence 9, Appli
768	333.5	18.8	289	14	US-10-436-523-88	Sequence 88, Appli
769	330.5	18.7	289	14	US-10-220-946-18	Sequence 18, Appli
770	330.5	18.7	289	14	US-10-436-523-76	Sequence 76, Appli
771	330.5	18.7	289	14	US-10-436-523-91	Sequence 91, Appli
772	330.5	18.7	289	15	US-10-170-385-131	Sequence 131, App
773	327.5	18.5	289	14	US-10-436-523-89	Sequence 89, Appli
774	327.5	18.5	289	14	US-10-436-523-90	Sequence 90, Appli
775	327	18.5	270	14	US-10-436-523-77	Sequence 77, Appli
776	319.5	18.0	331	14	US-10-436-523-39	Sequence 39, Appli
777	318	17.9	615	17	US-10-659-004-48	Sequence 48, Appli
778	318	17.9	654	14	US-10-104-943-7	Sequence 7, Appli
779	318	17.9	654	16	US-10-310-612-2	Sequence 2, Appli
780	318	17.9	654	16	US-10-328-538-2	Sequence 2, Appli
781	316.5	17.9	331	15	US-10-327-413-2	Sequence 2, Appli
782	315.5	17.8	309	14	US-10-436-523-5	Sequence 5, Appli
783	315.5	17.8	331	14	US-10-104-943-2	Sequence 2, Appli
784	315.5	17.8	331	15	US-10-436-523-3	Sequence 3, Appli
785	315.5	17.8	331	15	US-10-264-237-2559	Sequence 2559, Ap
786	315.5	17.8	331	16	US-10-614-853-22	Sequence 22, Appli
787	315.5	17.8	346	15	US-10-257-174-33	Sequence 33, Appli
788	314.5	17.7	331	14	US-10-436-523-41	Sequence 41, Appli
789	313.5	17.7	331	14	US-10-436-523-40	Sequence 40, Appli
790	312.5	17.6	610	10	US-09-860-836B-11	Sequence 11, Appli
791	311.5	17.6	331	14	US-10-436-523-42	Sequence 42, Appli
792	311	17.6	331	17	US-10-311-829-10	Sequence 10, Appli
801	311	17.6	332	14	US-10-237-535-76	Sequence 76, Appli
810	311	17.6	332	14	US-10-239-196-76	Sequence 76, Appli
824	311	17.6	332	14	US-10-104-943-41	Sequence 41, Appli
827	311	17.6	332	14	US-10-136-574-2	Sequence 2, Appli
903	311	17.6	332	15	US-10-471-449-5	Sequence 5, Appli
904	311	17.6	332	17	US-10-311-829-4	Sequence 4, Appli
905	307.5	17.4	285	14	US-10-436-523-100	Sequence 100, App
906	301.5	17.0	236	14	US-10-436-523-82	Sequence 82, Appli
907	298	16.8	217	14	US-10-436-523-79	Sequence 79, Appli
908	294.5	16.6	551	15	US-10-471-449-8	Sequence 8, Appli
909	282.5	15.9	526	17	US-10-659-004-50	Sequence 50, Appli
910	251	14.2	220	15	US-10-257-174-32	Sequence 32, Appli
911	247	13.9	310	15	US-10-258-951-48	Sequence 48, Appli
912	245	13.8	195	14	US-10-436-523-15	Sequence 15, Appli
913	245	13.8	203	14	US-10-436-523-16	Sequence 16, Appli
914	236.5	13.3	229	15	US-10-258-951-47	Sequence 47, Appli
915	235.5	12.7	331	9	US-10-436-523-11	Sequence 11, Appli
916	225.5	12.7	351	9	US-09-745-605-5	Sequence 5, Appli
917	225.5	12.7	351	14	US-10-104-943-3	Sequence 3, Appli
918	219	12.4	168	15	US-10-264-237-1621	Sequence 1621, Ap
919	206	11.6	220	14	US-10-104-943-43	Sequence 43, Appli
920	200.5	11.3	159	14	US-10-436-523-8	Sequence 8, Appli
921	199.5	11.3	221	15	US-10-471-449-4	Sequence 4, Appli
922	190.5	10.8	275	13	US-10-087-192-1485	Sequence 1485, Ap
923	182.5	10.3	335	9	US-09-731-449-20	Sequence 20, Appli
924	182.5	10.3	335	10	US-09-918-715-285	Sequence 285, App
925	182.5	10.3	335	10	US-09-369-248-3	Sequence 3, Appli
926	182.5	10.3	335	10	US-09-860-836B-1	Sequence 1, Appli
927	182.5	10.3	335	14	US-10-062-523-3	Sequence 3, Appli
928	182.5	10.3	335	14	US-10-254-426-20	Sequence 20, Appli

929	182.5	10.3	335	14	US-10-436-523-64	Sequence 64, Appl	1002	136.5	7.7	351	11	US-09-836-544-3	Sequence 3, Appli
930	182.5	10.3	335	15	US-10-464-469-3	Sequence 3, Appli	1003	136.5	7.7	351	13	US-10-087-192-1848	Sequence 1848, Ap
931	182.5	10.3	335	15	US-10-445-888A-3	Sequence 3, Appli	1004	136.5	7.7	351	14	US-10-329-599-6	Sequence 6, Appli
932	182.5	10.3	335	16	US-10-474-794-285	Sequence 285, App	1005	136.5	7.7	351	16	US-10-778-373-6	Sequence 6, Appli
933	182.5	10.3	335	17	US-10-882-171-3	Sequence 3, Appli	1006	136.5	7.7	351	16	US-10-470-764-6	Sequence 6, Appli
934	182.5	10.3	335	18	US-10-979-159-285	Sequence 285, App	1007	136.5	7.7	360	14	US-10-436-523-65	Sequence 65, Appl
935	179	10.1	278	9	US-09-731-449-25	Sequence 25, Appl	1471	134.5	7.6	198	14	US-10-174-587-502	Sequence 502, App
936	179	10.1	278	14	US-10-254-426-25	Sequence 25, Appl							
937	177.5	10.0	258	9	US-09-731-449-28	Sequence 28, Appl							
938	177.5	10.0	258	14	US-10-254-426-28	Sequence 28, Appl							
939	175	9.9	33	9	US-09-984-245-244	Sequence 244, App							
940	175	9.9	33	10	US-09-966-262-244	Sequence 244, App							
941	175	9.9	33	10	US-09-983-966-244	Sequence 244, App							
942	175	9.9	33	14	US-10-059-395-244	Sequence 244, App							
943	175	9.9	33	14	US-10-143-090-244	Sequence 244, App							
944	175	9.9	33	17	US-10-960-251-244	Sequence 244, App							
945	170	9.6	365	10	US-09-860-836B-5	Sequence 5, Appli							
946	170	9.6	365	14	US-10-436-523-59	Sequence 59, Appl							
947	170	9.6	391	15	US-10-264-049-2579	Sequence 2579, Ap							
948	164.5	9.3	305	10	US-09-918-715-286	Sequence 286, App							
949	164.5	9.3	305	16	US-10-474-794-286	Sequence 286, App							
950	164.5	9.3	305	18	US-10-979-159-286	Sequence 286, App							
951	158.5	8.9	329	10	US-09-860-836B-3	Sequence 3, Appli							
952	152	8.6	298	10	US-09-918-715-287	Sequence 287, App							
953	152	8.6	298	16	US-10-474-794-287	Sequence 287, App							
954	152	8.6	298	18	US-10-979-159-287	Sequence 287, App							
955	150.5	8.5	285	9	US-09-799-777-9	Sequence 9, Appli							
956	150.5	8.5	285	9	US-09-745-605-6	Sequence 6, Appli							
957	150.5	8.5	285	10	US-09-369-248-2	Sequence 2, Appli							
958	150.5	8.5	285	14	US-10-062-523-2	Sequence 2, Appli							
959	150.5	8.5	285	14	US-10-220-946-12	Sequence 12, Appl							
960	150.5	8.5	285	14	US-10-436-523-63	Sequence 63, Appl							
961	150.5	8.5	285	15	US-10-464-469-2	Sequence 2, Appli							
962	150.5	8.5	285	15	US-10-445-888A-2	Sequence 2, Appli							
963	150.5	8.5	285	16	US-10-755-889-158	Sequence 158, App							
964	150.5	8.5	285	16	US-10-723-860-3981	Sequence 3981, Ap							
965	150.5	8.5	285	17	US-10-892-171-2	Sequence 2, Appli							
966	150.5	8.5	285	17	US-10-491-997-158	Sequence 158, App							
967	146.5	8.3	211	9	US-09-731-449-29	Sequence 29, Appl							
968	146.5	8.3	211	14	US-10-254-426-29	Sequence 29, Appl							
969	146	8.2	312	14	US-09-731-449-5	Sequence 5, Appli							
970	146	8.2	312	9	US-10-254-426-5	Sequence 5, Appli							
971	146	8.2	320	9	US-09-731-449-37	Sequence 37, Appl							
972	146	8.2	320	14	US-10-254-426-37	Sequence 37, Appl							
973	144.5	8.2	285	9	US-09-731-449-45	Sequence 45, Appl							
974	144.5	8.2	285	14	US-10-254-426-45	Sequence 45, Appl							
975	144	8.1	358	13	US-10-087-192-1845	Sequence 1845, Ap							
976	142.5	8.0	416	16	US-10-706-691-16	Sequence 16, Appl							
977	142.5	8.0	416	16	US-10-706-691-41	Sequence 41, Appl							
978	141	8.0	149	10	US-09-983-802-443	Sequence 443, App							
979	141	8.0	149	10	US-09-984-490-443	Sequence 443, App							
980	141	8.0	149	11	US-09-973-278-571	Sequence 571, App							
981	140.5	7.9	142	11	US-09-973-278-252	Sequence 252, App							
982	140.5	7.9	143	10	US-09-983-802-192	Sequence 192, App							
983	140.5	7.9	143	10	US-09-984-490-192	Sequence 192, App							
984	140.5	7.9	290	9	US-09-731-449-13	Sequence 13, Appl							
985	140.5	7.9	290	14	US-10-254-426-13	Sequence 13, Appl							
986	140.5	7.9	298	9	US-09-731-449-40	Sequence 40, Appl							
987	140.5	7.9	298	14	US-10-254-426-40	Sequence 40, Appl							
988	139	7.8	28	9	US-09-984-245-243	Sequence 243, App							
989	139	7.8	28	10	US-09-966-262-243	Sequence 243, App							
990	139	7.8	28	10	US-09-983-966-243	Sequence 243, App							
991	139	7.8	28	14	US-10-059-395-243	Sequence 243, App							
992	139	7.8	28	14	US-10-143-090-243	Sequence 243, App							
993	139	7.8	28	17	US-10-960-251-243	Sequence 243, App							
994	139	7.8	263	9	US-09-731-449-48	Sequence 48, Appl							
995	139	7.8	263	14	US-10-254-426-48	Sequence 48, Appl							
996	138.5	7.8	418	16	US-10-706-691-18	Sequence 18, Appl							
997	138	7.8	70	14	US-10-436-523-97	Sequence 97, Appl							
998	137.5	7.8	383	16	US-10-706-691-26	Sequence 26, Appl							
999	136.5	7.7	327	16	US-10-657-006-7	Sequence 7, Appli							
1000	136.5	7.7	351	9	US-09-796-033-6	Sequence 6, Appli							
1001	136.5	7.7	351	9	US-09-730-465-6	Sequence 6, Appli							

Search completed: July 14, 2005, 13:32:58

Job time : 78 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 14, 2005, 13:22:13 ; Search time 20 seconds  
(without alignments)  
1611.631 Million cell updates/sec

Title: US-10-063-551-46

Perfect score: 1772

Sequence: 1 MAGSPTCLTLIIVLWLTGS.....PHSLLTMDPTPLFAVENVI 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	343	19.4	629	2 A46500	Ly-9.2 antigen - m
2	182.5	10.3	335	2 S58892	signaling lymphocy
3	144	8.1	344	2 B28967	T-cell surface gly
4	138	7.8	344	2 I49585	CD2 antigen protei
5	136.5	7.7	351	1 RWHUC2	T-cell surface gly
6	134	7.6	240	2 S01299	OX-45 membrane gly
7	130	7.3	344	1 RWRTC2	T-cell surface gly
8	126.5	7.1	240	2 JL0143	antigen BCM1 precu
9	125.5	7.1	321	2 JH0395	biliary glycoprote
10	125.5	7.1	351	2 JH0396	biliary glycoprote
11	125.5	7.1	417	2 JH0394	biliary glycoprote
12	125.5	7.1	464	2 C30127	transmembrane carc
13	125.5	7.1	526	1 A32164	biliary glycoprote
14	124.5	7.0	344	2 A27681	nonspecific cross-
15	122.5	6.9	521	2 S34338	biliary glycoprote
16	119	6.7	458	2 JCI509	biliary glycoprote
17	114.5	6.5	702	2 A36319	carcinoembryonic a
18	113.5	6.4	458	1 WMSR1	biliary glycoprote
19	113.5	6.4	521	2 JCI508	biliary glycoprote
20	109.5	6.2	432	2 S30193	T-cell surface gly
21	108.5	6.1	365	2 JC7780	coxsackie- and ade
22	107.5	6.1	398	2 I49443	gene 284 protein -
23	106	6.0	897	2 G84613	hypothetical prote
24	105.5	6.0	329	1 A48754	B7-2 antigen - hum
25	104	5.9	349	2 A34815	carcinoembryonic a
26	102.5	5.8	458	2 S23969	cell-adhesion mole
27	102.5	5.8	526	2 A37821	butyrophilin - bov
28	101.5	5.7	761	2 T00940	hypothetical prote
29	101	5.7	587	2 JH0464	DM-GRASP precursor

30	101	5.7	588	2 JH0506	adhesion molecule
31	100.5	5.7	259	2 A86822	hypothetical prote
32	100	5.6	392	2 B44194	poliovirus recepto
33	99	5.6	417	2 A44194	poliovirus recepto
34	99	5.6	588	2 A45254	surface glycoprote
35	98.5	5.6	1227	2 T23004	hypothetical prote
36	98	5.5	347	2 S41638	T-cell surface gly
37	98	5.5	503	2 JCS287	SHP substrate-1 pr
38	97	5.5	523	2 I50478	neurotin - goldfis
39	97	5.5	773	1 QRRBG	secretory componen
40	96.5	5.4	402	2 A40678	T-cell adhesion re
41	96	5.4	210	2 S36297	T-cell receptor ga
42	96	5.4	526	2 S70587	butyrophilin precu
43	96	5.4	1087	2 I51552	platelet-derived g
44	96	5.4	1451	2 S42167	190K protein - hum
45	95.5	5.4	341	2 JCI512	biliary glycoprote
46	95.5	5.4	417	1 RWHUPA	poliovirus recepto
47	95.5	5.4	458	2 S68177	C-CAM2a protein is
48	95.5	5.4	519	2 A44783	ecto-ATPase precu
49	95.5	5.4	700	1 S12053	protein-tyrosine-p
50	94.5	5.3	218	2 A36198	T-cell receptor be
51	94	5.3	233	2 JH0372	42K surface glycop
52	94	5.3	1088	1 IJXLNL	neural cell adhesi
53	93.5	5.3	2409	1 A60979	versican precursor
54	93	5.2	419	2 B54312	pregnancy-specific
55	93	5.2	419	2 A36109	pregnancy-specific
56	93	5.2	419	2 JCI4123	pregnancy-specific
57	92.5	5.2	299	2 S56749	functional adhesio
58	92.5	5.2	330	2 I46691	CD86 precursor - r
59	92.5	5.2	761	2 A96810	probable Mutator-1
60	92	5.2	822	2 T01095	hypothetical prote
61	91.5	5.2	1079	2 T28197	probable DNA-direc
62	91	5.1	417	2 A28277	pregnancy-specific
63	91	5.1	419	2 A33258	pregnancy-specific
64	91	5.1	426	2 B33258	pregnancy-specific
65	91	5.1	467	1 HLMSP3	poliovirus recepto
66	90	5.1	250	2 A28564	lymphocyte functio
67	90	5.1	395	2 D43354	pregnancy-specific
68	90	5.1	397	2 C43354	pregnancy-specific
69	90	5.1	406	2 B43354	pregnancy-specific
70	90	5.1	419	2 A31135	pregnancy-specific
71	90	5.1	426	2 A35964	pregnancy-specific
72	90	5.1	426	2 A35341	pregnancy-specific
73	90	5.1	428	2 A27658	pregnancy-specific
74	89.5	5.1	243	2 A53244	leukocyte antigen
75	89.5	5.1	349	2 E84968	outer membrane pro
76	89.5	5.1	428	2 T36565	probable penicilli
77	89	5.0	309	2 I49522	gene B7-2 protein
78	89	5.0	341	2 JCI511	biliary glycoprote
79	89	5.0	821	1 C1RHU3	calpain (EC 3.4.22
80	89	5.0	5175	2 T20992	hypothetical prote
81	89	5.0	5198	2 T43290	hemocytin precurs
82	88.5	5.0	1390	1 TVHUME	UDP-N-acetylglucos
83	88	5.0	363	2 F70195	hypothetical prote
84	88	5.0	422	2 A71147	poliovirus recepto
85	88	5.0	530	2 A53437	polymyxin B resiat
86	88	5.0	668	2 S56909	protein-tyrosine-p
87	88	5.0	699	2 JCI6132	calpain (EC 3.4.22
88	88	5.0	821	1 B34488	neural cell adhesi
89	88	5.0	1092	1 JN0635	nebulin, skeletal
90	88	5.0	6669	2 S55024	carcinoembryonic a
91	87.5	4.9	276	2 A5811	31.6K hypothetical
92	87.5	4.9	265	2 S20690	poliovirus recepto
93	87.5	4.9	392	1 RWHUPD	secretory componen
94	87.5	4.9	769	1 ORRTGS	kinase-related pro
95	87.5	4.9	2340	2 I48310	connectin/titin -
96	87.5	4.9	4162	2 T42633	T-cell surface gly
97	87	4.9	457	1 RWMST4	alcam - human
98	87	4.9	583	2 I39428	skelemin - mouse
99	87	4.9	1666	2 A48594	protein-tyrosine-p
100	87	4.9	1907	2 S50893	heparan sulfate pr
101	87	4.9	3707	2 S18252	extracellular solu
102	86.5	4.9	528	2 B75364	

103	86	4.9	212	2	C33258	pregnancy-specific	176	80	4.5	1040	2	A49356	transient axonal g
104	86	4.9	354	1	VBEB67	glycoprotein D pre	177	80	4.5	1170	2	A40558	thrombospondin 1 p
105	86	4.9	428	2	I57486	pregnancy-specific	178	79.5	4.5	134	2	I46627	rearranged T-cell
106	86	4.9	885	2	B86257	NBS/LRR disease re	179	79.5	4.5	244	2	JC8019	CD58 protein - pig
107	86	4.9	1327	2	T09402	immunoglobulin-lik	180	79.5	4.5	249	1	A61087	myelin P0 glycopro
108	85.5	4.8	324	2	G43354	pregnancy-specific	181	79.5	4.5	273	2	B28928	pregnancy-specific
109	85.5	4.8	326	2	F43354	pregnancy-specific	182	79.5	4.5	275	2	A28928	pregnancy-specific
110	85.5	4.8	333	2	A43354	pregnancy-specific	183	79.5	4.5	282	2	C28928	pregnancy-specific
111	85.5	4.8	335	2	H43354	pregnancy-specific	184	79.5	4.5	289	2	G90314	oxidoreductase (im
112	85.5	4.8	941	1	TVMVMD	protein-tyrosine k	185	79.5	4.5	328	2	JQ1121	cysteine proteinas
113	85.5	4.8	2588	2	T14342	NSD1 protein - mou	186	79.5	4.5	400	2	A10104	probable Galactosi
114	85	4.8	428	2	JS0032	pregnancy-specific	187	79.5	4.5	430	2	T28143	tapasin 1 homolog,
115	85	4.8	731	2	T16524	hypothetical prote	188	79.5	4.5	446	2	T34782	probable signal pe
116	85	4.8	757	1	S48841	secretory componen	189	79.5	4.5	490	2	I41293	Ecog type I restri
117	84.5	4.8	656	2	A96724	hypothetical prote	190	79.5	4.5	769	2	S16236	fibroblast growth
118	84	4.7	275	2	JC7604	CD86 spliced varia	191	79.5	4.5	822	2	A45081	fibroblast growth
119	84	4.7	851	2	D90216	hypothetical prote	192	79.5	4.5	822	2	A41794	keratinocyte growt
120	84	4.7	1379	1	S01254	hepatocyte growth	193	79.5	4.5	873	1	I48952	VLDL receptor prec
121	84	4.7	1499	2	I50212	protein-tyrosine-p	194	79.5	4.5	980	1	TVCIMD	macrophage colony-
122	84	4.7	3034	2	T14119	seven-pass transme	195	79.5	4.5	1465	2	S43529	165K protein, skel
123	83.5	4.7	315	2	H71009	probable prolifera	196	79.5	4.5	2491	1	A28372	insulin-like growt
124	83.5	4.7	392	2	T33444	hypothetical prote	197	79	4.5	210	2	C87256	hypothetical prote
125	83.5	4.7	656	2	B49423	senaphorin I - fru	198	79	4.5	244	2	AC1765	B. subtilis TagA p
126	83.5	4.7	775	2	T21436	hypothetical prote	199	79	4.5	438	2	G64513	hypothetical prote
127	83.5	4.7	1501	2	I58148	protein-tyrosine-p	200	79	4.5	479	2	G84039	carboxy-terminal p
128	83.5	4.7	1863	2	S46217	protein-tyrosine-p	201	79	4.5	584	2	T08678	hypothetical prote
129	83	4.7	335	2	A33514	pregnancy-specific	202	79	4.5	657	2	S77543	short-chain alcoh
130	83	4.7	757	2	I45956	polymERIC immunog	203	79	4.5	903	2	T20804	hypothetical prote
131	83	4.7	873	1	A49729	VLDL receptor prec	204	79	4.5	1228	2	G96751	hypothetical prote
132	83	4.7	925	2	T37475	lipoprotein recept	205	79	4.5	1361	2	T30884	neural specific DN
133	83	4.7	1106	2	T29496	hypothetical prote	206	78.5	4.4	235	2	S25750	ig lambda chain -
134	83	4.7	2489	2	S59782	probable membrane	207	78.5	4.4	429	1	EHRT	ig epsilon chain C
135	82.5	4.7	393	2	B96780	hypothetical prote	208	78.5	4.4	497	2	C91225	probable oxidoredu
136	82.5	4.7	826	2	B36203	iron-responsive el	209	78.5	4.4	497	2	A86072	probable oxidoredu
137	82.5	4.7	1004	2	A71617	SERA antigen/papai	210	78.5	4.4	539	2	T01513	Ctp synthase (EC 6
138	82.5	4.7	2626	1	I38344	ctitin, cardiac mus	211	78.5	4.4	588	2	T37202	B-CAM protein - hu
139	82	4.6	386	2	B69666	Na+ ABC transporte	212	78.5	4.4	628	2	I38000	Lutheran blood gro
140	82	4.6	609	2	S43009	hemagglutinin - ri	213	78.5	4.4	638	2	T51383	receptor protein k
141	82	4.6	880	2	B33743	protein-tyrosine k	214	78.5	4.4	831	2	S39835	hypothetical prote
142	82	4.6	3562	2	A47171	chondroitin sulfat	215	78.5	4.4	847	2	JH0371	B-cell adhesion pr
143	81.5	4.6	278	1	T0RT0X	OX-2 membrane glyc	216	78.5	4.4	1036	2	S22383	axonin 1 precursor
144	81.5	4.6	352	2	I77374	pregnancy-specific	217	78.5	4.4	1038	2	AG2187	hypothetical prote
145	81.5	4.6	355	2	T06122	cysteine proteinas	218	78.5	4.4	1468	2	T05672	hypothetical prote
146	81.5	4.6	378	2	S00842	leukosialin precu	219	78	4.4	257	2	A97121	undecaprenyl pyrop
147	81.5	4.6	497	2	D97264	galactose-1-phosph	220	78	4.4	272	2	I48268	biliary glycoprote
148	81.5	4.6	524	2	S44982	flagellin - Shigell	221	78	4.4	286	2	A28333	carcinoembryonic a
149	81.5	4.6	708	2	T48022	hypothetical prote	222	78	4.4	335	2	C54312	pregnancy-specific
150	81	4.6	335	2	B33251	nonspecific cross-	223	78	4.4	402	2	T09062	probable advanced
151	81	4.6	338	2	JC4776	limbic-system-asso	224	78	4.4	490	2	T43184	DEAD box ATP-depen
152	81	4.6	374	2	S57750	naringenin 3-dioxy	225	78	4.4	604	2	T41249	DEAD box ATP-depen
153	81	4.6	760	2	S19374	probable membrane	226	78	4.4	608	2	AB3562	gtp-binding protei
154	81	4.6	769	2	E97092	glycosyltransferas	227	78	4.4	609	1	HMNZKA	hemagglutinin - ri
155	81	4.6	829	1	IJHUCP	cadherin 3 precurs	228	78	4.4	761	1	IJHUNGA	neural cell adhesi
156	81	4.6	1898	2	S46216	leukocyte antigen-	229	78	4.4	836	2	T42323	hypothetical prote
157	81	4.6	1941	2	T30554	ubiquitin-protein	230	78	4.4	905	2	S43084	cadherin - African
158	80.5	4.5	346	2	S46993	elk ligand - human	231	78	4.4	905	2	T38314	probable vacuolar
159	80.5	4.5	376	2	E85435	cysteine proteinas	232	77.5	4.4	172	2	T34227	hypothetical prote
160	80.5	4.5	462	2	H97292	UDP-N-acetylmuramo	233	77.5	4.4	214	2	C98933	hypothetical prote
161	80.5	4.5	473	2	AG0612	probable transport	234	77.5	4.4	236	2	T41012	conserved hypothet
162	80.5	4.5	475	2	I76668	pregnancy-specific	235	77.5	4.4	239	2	I46082	CDB alpha-chain
163	80.5	4.5	540	2	B64829	membrane protein b	236	77.5	4.4	448	2	H98007	exodeoxyribonuclea
164	80.5	4.5	540	2	H90751	probable transport	237	77.5	4.4	509	2	JC5288	SHP substrate-1 pr
165	80.5	4.5	540	2	F85615	probable transport	238	77.5	4.4	513	2	JC5289	SHP substrate-1 pr
166	80.5	4.5	721	2	T09631	probable acylamino	239	77.5	4.4	539	2	G86465	F12G12.2 protein -
167	80.5	4.5	823	2	T08092	plus fringe glycop	240	77.5	4.4	591	2	H83362	gluconate dehydrog
168	80.5	4.5	343	2	S44887	ZK112.7 protein -	241	77.5	4.4	717	2	AD3037	ferrienterobactin-
169	80.5	4.5	642	2	T29757	protein UNC-89 - C	242	77.5	4.4	717	2	E98189	ferrienterobactin-
170	80	4.5	307	1	RWMSBC	T-cell receptor be	243	77.5	4.4	739	2	A41288	vascular cell adhe
171	80	4.5	341	2	I61725	natural killer aas	244	77.5	4.4	757	1	S64742	dynamatin-related pr
172	80	4.5	343	2	G90680	probable periplasm	245	77.5	4.4	863	2	S06017	neuraxin - rat
173	80	4.5	343	2	C85531	periplasmic ferric	246	77.5	4.4	881	2	S03068	env protein - huma
174	80	4.5	454	2	A46532	ig mu chain C regi	247	77.5	4.4	968	2	T25667	hypothetical prote
175	80	4.5	454	2	JH0110	arginine/ornithine	248	77.5	4.4	991	2	T48631	polynucleotide pho

249	77.5	4.4	1015	2	T32186	hypothetical prote	322	76	4.3	978	2	S16385	macrophage colony-
250	77.5	4.4	1099	2	T18713	hypothetical prote	323	76	4.3	1018	2	JC4211	neural adhesion pr
251	77.5	4.4	1205	2	T13959	timeless protein T	324	76	4.3	1093	2	TS1503	valine-crNA ligase
252	77.5	4.4	1262	1	B48758	protein-tyrosine-p	325	75.5	4.3	2029	1	TDFFLK	protein-tyrosine-p
253	77.5	4.4	1496	1	A48758	protein-tyrosine-p	326	75.5	4.3	246	2	A47712	myelin/oligodendro
254	77.5	4.4	1894	2	C54689	protein-tyrosine-p	327	75.5	4.3	326	2	JC4124	pregnancy-specific
255	77.5	4.4	1912	2	A56178	protein-tyrosine-p	328	75.5	4.3	419	2	S42989	T48 protein - frui
256	77.5	4.4	1950	2	S12332	ubiquitin-protein	329	75.5	4.3	421	2	T40614	G beta repeat prot
257	77	4.3	327	2	S06611	Ig gamma-2 chain C	330	75.5	4.3	432	2	T30130	hypothetical prote
258	77	4.3	328	2	I47158	Ig gamma 1 chain C	331	75.5	4.3	432	2	T30130	hypothetical prote
259	77	4.3	338	2	JC5519	50K glycoprotein p	332	75.5	4.3	446	2	A95140	exodeoxyribonuclea
260	77	4.3	398	2	B86353	protein F2R2.6 [im	333	75.5	4.3	462	2	A84689	chloroplast membra
261	77	4.3	439	2	S51378	probable membrane	334	75.5	4.3	485	2	T28076	hypothetical prote
262	77	4.3	491	2	J80276	voltage-gated pota	335	75.5	4.3	819	2	T05744	hypothetical prote
263	77	4.3	502	2	S61935	SKS1 protein - yea	336	75.5	4.3	933	2	H69045	hypothetical prote
264	77	4.3	523	2	T05946	cytochrome P450 78	337	75.5	4.3	1020	2	S05944	neuronal cell surf
265	77	4.3	796	2	JC7966	xylan 1,4-beta-xy	338	75	4.2	2109	1	I50421	aggregan precursor
266	77	4.3	873	1	QRREV7	VLDL receptor prec	339	75	4.2	208	2	D71529	hypothetical prote
267	77	4.3	1021	2	I39207	leukocyte surface	340	75	4.2	466	2	D84906	probable beta-keto
268	77	4.3	1029	2	D83120	probable RND efflu	341	75	4.2	491	2	AC2650	glucose-6-phosphat
269	77	4.3	1041	2	S55862	probable membrane	342	75	4.2	503	2	B97432	glucose-6-phosphat
270	77	4.3	1897	1	TDHULK	leukocyte antigen-	343	75	4.2	543	2	S26609	glutamate/aspartat
271	77	4.3	2167	2	AF1489	cell wall-associat	344	75	4.2	572	2	B46529	Ig y heavy chain (
272	77	4.3	4836	2	T14346	herc2 protein - mo	345	75	4.2	573	2	S12838	Ig mu chain precu
273	76.5	4.3	177	1	C40428	nonspecific cross-	346	75	4.2	622	2	B6751	hypothetical prote
274	76.5	4.3	191	2	E75132	molybdopterin-guan	347	75	4.2	686	2	A56665	microtubule-associ
275	76.5	4.3	238	2	T24314	hypothetical prote	348	75	4.2	747	1	QRECFE	ferrichrome-iron r
276	76.5	4.3	251	2	S75312	hypothetical prote	349	75	4.2	747	2	B85499	outer membrane rec
277	76.5	4.3	296	2	G82131	conserved hypothet	350	75	4.2	747	2	B90648	outer membrane rec
278	76.5	4.3	390	2	D86291	hypothetical prote	351	75	4.2	821	1	TVMSBK	fibroblast growth
279	76.5	4.3	394	2	S20905	hypothetical prote	352	75	4.2	976	1	TVMSMD	macrophage colony-
280	76.5	4.3	402	2	A54312	pregnancy-specific	353	75	4.2	1091	1	IUCHNL	neural cell adhesi
281	76.5	4.3	423	2	AB1142	N-carbamyl-L-amino	354	75	4.2	1256	2	T03096	CDO protein - rat
282	76.5	4.3	426	2	C55181	pregnancy-specific	355	75	4.2	1338	2	T02206	hypothetical prote
283	76.5	4.3	426	2	S09016	pregnancy-specific	356	75	4.2	1338	2	I38346	elastic titin - hu
284	76.5	4.3	426	2	B35334	pregnancy-specific	357	74.5	4.2	232	1	DXCH	ovalbumin-related
285	76.5	4.3	436	2	B55181	pregnancy-specific	358	74.5	4.2	278	2	A39037	carcinoembryonic a
286	76.5	4.3	495	2	A55181	pregnancy-specific	359	74.5	4.2	309	2	T31908	hypothetical prote
287	76.5	4.3	497	2	D65189	yigC protein - Esc	360	74.5	4.2	321	2	S10006	hypothetical prote
288	76.5	4.3	582	2	A71906	DNA polymerase III	361	74.5	4.2	379	2	D91078	probable lipoprote
289	76.5	4.3	727	2	T23585	hypothetical prote	362	74.5	4.2	379	2	E85923	lipoprotein (impor
290	76.5	4.3	788	2	S17906	hypothetical prote	363	74.5	4.2	379	2	B55522	lipoprotein D prec
291	76.5	4.3	839	2	B96538	hypothetical prote	364	74.5	4.2	463	2	T14884	hypothetical prote
292	76.5	4.3	876	2	S71277	serine/threonine-s	365	74.5	4.2	518	2	D69539	conserved hypothet
293	76.5	4.3	876	2	D85350	hypothetical prote	366	74.5	4.2	544	2	I51593	protein-tyrosine k
294	76.5	4.3	1005	2	T18537	Ig heavy chain - c	367	74.5	4.2	688	2	A47705	triacylglycerol li
295	76.5	4.3	1043	2	T19734	hypothetical prote	368	74.5	4.2	705	2	S51635	fibroblast growth
296	76.5	4.3	1071	2	T18307	suppressor protein	369	74.5	4.2	741	2	F90739	probable transport
297	76.5	4.3	1089	1	PFHUGA	platelet-derived g	370	74.5	4.2	741	2	H85589	probable transport
298	76.5	4.3	1124	2	JX0293	zinc finger protei	371	74.5	4.2	764	2	A49448	irregular chiasm C
299	76.5	4.3	1154	2	A56242	E-box-binding repr	372	74.5	4.2	771	2	T34376	hypothetical prote
300	76.5	4.3	1328	2	S62467	ATP-dependent DNA	373	74.5	4.2	786	2	H64817	probable membrane
301	76.5	4.3	1461	2	B70588	probable polyketid	374	74.5	4.2	795	2	T20609	hypothetical prote
302	76.5	4.3	1802	2	S69703	HKR1 protein precu	375	74.5	4.2	889	1	VCLJG5	env polyprotein -
303	76.5	4.3	2039	2	T15347	ankyrin-related un	376	74.5	4.2	984	2	T00326	hypothetical prote
304	76	4.3	138	2	S16199	photosystem I prot	377	74.5	4.2	1003	2	T19638	hypothetical prote
305	76	4.3	144	2	AH1172	mannose-specific p	378	74.5	4.2	1007	2	PN0156	hypothetical prote
306	76	4.3	230	2	S49449	Ig lambda chain -	379	74.5	4.2	1008	2	S28858	glutamate receptor
307	76	4.3	239	2	T23147	hypothetical prote	380	74.5	4.2	1021	2	A57112	contactin precursor
308	76	4.3	262	2	A64882	probable carboxype	381	74.5	4.2	1178	2	E87145	[beta] subunit of
309	76	4.3	262	2	H85751	probable carboxype	382	74.5	4.2	1179	2	S31145	DNA-directed RNA p
310	76	4.3	262	2	A99867	probable carboxype	383	74.5	4.2	1522	2	T00028	brain-specific ang
311	76	4.3	286	2	B97010	prephenate dehydro	384	74.5	4.2	1723	2	S58880	receptor DEC-205 -
312	76	4.3	305	2	H63759	conserved hypothet	385	74.5	4.2	1896	2	T08851	Down syndrome cell
313	76	4.3	333	2	A31923	amalgam protein pr	386	74.5	4.2	2256	2	AD1018	large repetitive p
314	76	4.3	378	2	I46268	brevican precursor	387	74.5	4.2	2364	2	A56577	microtubule-associ
315	76	4.3	487	1	S55194	DNA-directed DNA p	388	74.5	4.2	2783	2	T34416	hypothetical prote
316	76	4.3	507	2	T47021	hypothetical prote	389	74	4.2	2803	2	S36291	T-cell receptor ga
317	76	4.3	508	2	AD0236	L-asparagine perme	390	74	4.2	234	2	S01320	Ig kappa chain pre
318	76	4.3	550	2	G90497	hypothetical prote	391	74	4.2	278	2	JC1506	biliary glycoprote
319	76	4.3	758	2	T15577	hypothetical prote	392	74	4.2	333	2	PS0018	Ig gamma-2b chain
320	76	4.3	841	2	T01011	hypothetical prote	393	74	4.2	334	2	T19637	hypothetical prote
321	76	4.3	964	2	T15746	hypothetical prote	394	74	4.2	349	2	S68092	protein-glutamine

395	74	4.2	384	2	H64161	hypothetical prote	468	73	4.1	3788	2	T30851	lysosomal traffick
396	74	4.2	403	2	I52590	m33-B isoform - mo	469	72.5	4.1	202	2	T36293	t-cell receptor ga
397	74	4.2	424	2	T43498	hypothetical prote	470	72.5	4.1	221	2	T31620	hypothetical prote
398	74	4.2	463	2	C69997	probable proline t	471	72.5	4.1	334	2	G01650	malate dehydrogena
399	74	4.2	468	2	S70297	SP82 protein homol	472	72.5	4.1	336	2	C27658	pregnancy-specific
400	74	4.2	502	2	T40792	hypothetical prote	473	72.5	4.1	342	2	AG1729	protein gp19 (Bact
401	74	4.2	548	2	A44302	protein-glutamine	474	72.5	4.1	351	2	B34595	pregnancy-specific
402	74	4.2	586	2	T15259	hypothetical prote	475	72.5	4.1	363	2	T39726	mannopine biosynth
403	74	4.2	611	2	F82442	probable peptide A	476	72.5	4.1	371	2	T40287	hypothetical prote
404	74	4.2	645	2	T39614	kinase-binding pro	477	72.5	4.1	377	2	B90437	hypothetical prote
405	74	4.2	673	2	T48701	hypothetical prote	478	72.5	4.1	399	2	A11114	surface protein (p
406	74	4.2	860	2	JC5702	ErB8 kinase activa	479	72.5	4.1	424	2	A34595	pregnancy-specific
407	74	4.2	862	2	I49583	differentiation an	480	72.5	4.1	435	2	D33258	pregnancy-specific
408	74	4.2	876	2	B96693	probable receptor	481	72.5	4.1	440	2	S52895	TYA protein - yea
409	74	4.2	900	2	G96617	probable disease r	482	72.5	4.1	443	2	AE3294	tolB protein [impo
410	74	4.2	1063	2	A33830	cation efflux syst	483	72.5	4.1	478	2	A49228	trypsin-like prote
411	74	4.2	1063	2	JC4700	cadmium, zinc, cob	484	72.5	4.1	487	2	A11146	hypothetical cell
412	74	4.2	1130	2	T23104	hypothetical prote	485	72.5	4.1	491	2	T22844	hypothetical prote
413	74	4.2	1133	2	T23103	hypothetical prote	486	72.5	4.1	527	2	D75127	hypothetical prote
414	74	4.2	1165	1	S45879	chitin synthase (E	487	72.5	4.1	666	2	A39610	SLY1 protein - yea
415	74	4.2	1237	2	E86457	probable RNA helic	488	72.5	4.1	682	2	A35969	heparin-binding gr
416	74	4.2	1367	2	T33819	hypothetical prote	489	72.5	4.1	687	2	T39838	hypothetical prote
417	74	4.2	1582	2	T15308	hypothetical prote	490	72.5	4.1	768	2	JC7352	glucose-regulated
418	74	4.2	4344	1	A53489	dynein heavy chain	491	72.5	4.1	769	2	T45854	hypothetical prote
419	74	4.2	5332	2	A45086	HC-toxin synthetas	492	72.5	4.1	842	2	E96641	hypothetical prote
420	74	4.2	6658	2	T13931	projectin - fruit	493	72.5	4.1	851	2	S44890	ncl-1 ZK112.2 prot
421	73.5	4.1	325	2	S49451	cysteine proteinas	494	72.5	4.1	876	2	A49508	protein-tyrosine k
422	73.5	4.1	364	2	A30521	myeloid cell surfa	495	72.5	4.1	895	2	T11979	Preprotein translo
423	73.5	4.1	428	2	B83967	dihydroorotase pyr	496	72.5	4.1	913	2	A48280	receptor tyrosine
424	73.5	4.1	647	2	T33773	hypothetical prote	497	72.5	4.1	1057	2	S45801	probable membrane
425	73.5	4.1	740	2	AH0600	probable membrane	498	72.5	4.1	1123	2	AB0123	exodeoxyribonuclea
426	73.5	4.1	797	2	T27518	hypothetical prote	499	72.5	4.1	1138	2	A82939	membrane nucleate
427	73.5	4.1	850	2	JC5700	ErB8 kinase activa	500	72.5	4.1	1272	2	S26180	neurofascin - chic
428	73.5	4.1	880	1	VCLJ52	env polyprotein pr	501	72.5	4.1	1434	2	T30172	transmembrane prot
429	73.5	4.1	923	2	F84732	probable ligand-ga	502	72.5	4.1	1575	2	T18545	lysobactin synthet
430	73.5	4.1	926	2	D83888	glucan 1,4-beta-gl	503	72.5	4.1	4367	1	B54802	dynein heavy chain
431	73.5	4.1	957	2	C69463	type I restriction	504	72.5	4.1	4924	2	T50176	probable pepide s
432	73.5	4.1	1166	2	T37692	probable tumor sup	505	72.5	4.1	4936	2	AH2515	hypothetical prote
433	73.5	4.1	1225	2	S48251	ubiquitin-protein	506	72	4.1	265	2	H72233	purine nucleoside
434	73.5	4.1	1240	2	T03097	CDO protein - huma	507	72	4.1	320	2	C99867	hypothetical prote
435	73.5	4.1	2013	2	AD1129	probable peptidogl	508	72	4.1	378	2	T51237	scarcrow-like pro
436	73.5	4.1	2042	2	T18399	variant-specific s	509	72	4.1	423	2	T29549	hypothetical prote
437	73.5	4.1	2301	1	GNNTN	genome polyprotein	510	72	4.1	437	2	AF3613	hypothetical prote
438	73.5	4.1	3255	2	G81702	adherence factor T	511	72	4.1	442	2	E71523	hypothetical prote
439	73.5	4.1	4544	1	S02392	alpha-2-macroglobu	512	72	4.1	446	2	B89922	conserved hypothet
440	73	4.1	147	2	T34265	hypothetical prote	513	72	4.1	469	2	C69628	gamma-aminobutyrat
441	73	4.1	220	1	G69047	conserved hypothet	514	72	4.1	506	2	F69867	two-component sens
442	73	4.1	235	2	S14675	Ig lambda chain -	515	72	4.1	510	2	A84707	probable pseudouri
443	73	4.1	250	2	S27544	hypothetical prote	516	72	4.1	521	2	E82377	ABC transporter, p
444	73	4.1	293	2	H96906	hypothetical prote	517	72	4.1	543	2	S38353	glutamate transpor
445	73	4.1	322	2	H84095	hypothetical prote	518	72	4.1	549	2	T33517	hypothetical prote
446	73	4.1	354	2	T27712	hypothetical prote	519	72	4.1	558	2	T01343	hypothetical prote
447	73	4.1	389	2	T46722	conserved hypothet	520	72	4.1	565	2	C82280	sensor kinase citA
448	73	4.1	397	2	E86304	F611.9 protein - A	521	72	4.1	585	2	S48929	hypothetical prote
449	73	4.1	413	2	S65948	hemolin - cecropia	522	72	4.1	599	2	T16774	hypothetical prote
450	73	4.1	413	2	A37778	hemolin precursor	523	72	4.1	617	2	T23197	hypothetical prote
451	73	4.1	432	1	RWMT4	T-cell surface gly	524	72	4.1	646	2	I38049	cell surface glyco
452	73	4.1	476	2	H84524	probable fatty aci	525	72	4.1	783	2	T45899	receptor protein k
453	73	4.1	519	2	S38921	hypothetical prote	526	72	4.1	808	2	F81180	conserved hypothet
454	73	4.1	590	2	I56526	interleukin 1 rece	527	72	4.1	868	2	JC5701	ErB8 kinase activa
455	73	4.1	666	1	A36026	kinesin-related pr	528	72	4.1	873	2	H96503	protein F9C16.17 [
456	73	4.1	730	2	S64998	hypothetical prote	529	72	4.1	885	2	D86151	F22M8.8 protein -
457	73	4.1	735	2	T00850	probable receptor-	530	72	4.1	900	2	T04839	protein kinase hom
458	73	4.1	853	1	IJBONC	neural cell adhesi	531	72	4.1	901	2	S07419	core protein p3 -
459	73	4.1	864	2	JH0438	penicillin-binding	532	72	4.1	911	2	B34721	androgen receptor
460	73	4.1	901	1	P3XR17	core protein VP3 -	533	72	4.1	1038	2	H90053	hypothetical prote
461	73	4.1	1014	2	T13476	hypothetical prote	534	72	4.1	1186	2	T19334	hypothetical prote
462	73	4.1	1072	2	A38457	integrin alpha-6 c	535	72	4.1	1214	2	JC7259	Smad interacting p
463	73	4.1	1171	2	T31635	hypothetical prote	536	72	4.1	1216	2	H85023	hypothetical prote
464	73	4.1	1179	2	T05673	hypothetical prote	537	72	4.1	1273	2	T42405	sax-3 protein - Ca
465	73	4.1	1515	1	S51863	cadmium resistance	538	72	4.1	1348	2	S51656	vascular endotheli
466	73	4.1	1737	2	A52235	unconventional myo	539	72	4.1	1906	1	S86235	myosin-light-chain
467	73	4.1	1806	2	T23298	hypothetical prote	540	72	4.1	2383	2	D64962	probable membrane

541	4.1	4872	2	S27272	614	71	4.0	1217	2	T22672	hypothetical prote
542	4.0	145	2	S25743	615	71	4.0	1251	2	T21389	hypothetical prote
543	4.0	229	1	B43685	616	71	4.0	1338	2	S09982	protein-tyrosine k
544	4.0	238	2	A49633	617	71	4.0	4391	2	A38096	perlecan precursor
545	4.0	299	2	S50803	618	71	4.0	5107	2	T29144	partial CDS - Caen
546	4.0	312	2	A64461	619	70.5	4.0	203	2	F69381	flagellin (flaB1-1
547	4.0	338	2	A64303	620	70.5	4.0	223	2	A81068	hypothetical prote
548	4.0	339	2	S09881	621	70.5	4.0	238	2	D86302	hypothetical prote
549	4.0	362	2	T05167	622	70.5	4.0	246	2	B82764	hypothetical prote
550	4.0	443	2	T14916	623	70.5	4.0	332	2	T45770	hypothetical prote
551	4.0	498	2	G90067	624	70.5	4.0	338	1	DETTMM	malate dehydrogena
552	4.0	500	2	T11946	625	70.5	4.0	358	2	E89588	protein R09F10.8 l
553	4.0	542	2	AF2587	626	70.5	4.0	429	1	B41902	arsenical pump mem
554	4.0	542	2	P97369	627	70.5	4.0	455	2	G01923	KIR (C1-5) NK rece
555	4.0	589	2	T50385	628	70.5	4.0	502	2	T19108	hypothetical prote
556	4.0	603	2	H84442	629	70.5	4.0	505	2	T15159	hypothetical prote
557	4.0	669	2	T48466	630	70.5	4.0	522	2	T26319	hypothetical prote
558	4.0	707	2	A38429	631	70.5	4.0	526	1	TVFV60	protein-tyrosine k
559	4.0	707	2	A54846	632	70.5	4.0	533	1	TVFV60	protein-tyrosine k
560	4.0	764	1	ORHUGS	633	70.5	4.0	537	1	A45501	protein-tyrosine k
561	4.0	822	2	B54846	634	70.5	4.0	545	2	S22313	protein-tyrosine k
562	4.0	919	2	S33942	635	70.5	4.0	546	2	S22314	protein-tyrosine k
563	4.0	921	2	F71486	636	70.5	4.0	557	1	TVFVS2	protein-tyrosine k
564	4.0	1032	2	H64100	637	70.5	4.0	558	1	MXRRRT	RNA 10 protein - r
565	4.0	1089	1	S33727	638	70.5	4.0	568	1	TVFVS1	protein-tyrosine k
566	4.0	1180	2	E86719	639	70.5	4.0	569	2	A45624	trophozoite cystei
567	4.0	1348	2	S27812	640	70.5	4.0	587	1	TVFVPR	protein-tyrosine k
568	4.0	1348	2	A43917	641	70.5	4.0	627	2	S14683	IG mu chain precu
569	4.0	1374	2	S62524	642	70.5	4.0	627	2	A69663	DNA mismatch repa
570	4.0	1377	2	C70148	643	70.5	4.0	630	2	A39344	tumor-associated m
571	4.0	1413	2	D84481	644	70.5	4.0	646	2	T48644	negative regulator
572	4.0	1462	2	T11648	645	70.5	4.0	656	2	H84206	acetyl-CoA synthet
573	4.0	2397	1	A55335	646	70.5	4.0	663	1	TVNVR	protein-tyrosine k
574	4.0	61	2	C82535	647	70.5	4.0	669	2	T13640	probable minor str
575	4.0	142	2	S38392	648	70.5	4.0	743	2	F71062	hypothetical prote
576	4.0	189	2	G64496	649	70.5	4.0	787	2	T41974	replication origin
577	4.0	201	2	T50206	650	70.5	4.0	793	2	T41703	dipeptidyl aminope
578	4.0	221	2	T21117	651	70.5	4.0	844	2	S05988	translation elonga
579	4.0	224	2	H81568	652	70.5	4.0	877	1	IUBOCN	N-cadherin precurs
580	4.0	231	2	B65520	653	70.5	4.0	878	2	S11842	hypothetical prote
581	4.0	231	2	G72102	654	70.5	4.0	895	2	A55413	triglyceride trans
582	4.0	258	2	S73803	655	70.5	4.0	906	1	IJWSCN	N-cadherin precurs
583	4.0	329	1	DEDFLM	656	70.5	4.0	928	2	G86546	polymorphic outer
584	4.0	333	2	AF0407	657	70.5	4.0	928	2	G81591	polymorphic membra
585	4.0	343	2	A10358	658	70.5	4.0	938	2	F86548	polymorphic outer
586	4.0	344	2	I56551	659	70.5	4.0	938	2	H72074	polymorphic membra
587	4.0	345	2	I48780	660	70.5	4.0	1088	2	B56715	calcium receptor (
588	4.0	346	2	AF1820	661	70.5	4.0	1200	2	T17404	hyalin - sea urchi
589	4.0	387	2	B71611	662	70.5	4.0	1356	2	JC1402	protein-tyrosine k
590	4.0	389	2	S68155	663	70.5	4.0	1402	2	F84480	probable retroelem
591	4.0	390	2	T27033	664	70.5	4.0	1427	2	I51669	tumor suppressor -
592	4.0	407	2	T34442	665	70.5	4.0	1694	2	S50065	sialoadhesin - mou
593	4.0	423	1	EHMS5	666	70.5	4.0	2051	2	T30938	receptor tyrosine
594	4.0	455	2	S50391	667	70.5	4.0	2303	1	GNNYTP	genome polyprotein
595	4.0	462	2	JN0719	668	70.5	4.0	2303	2	S13554	genome polyprotein
596	4.0	463	2	AH1758	669	70.5	4.0	2464	1	QRMSP1	microtubule-associ
597	4.0	509	1	WMVZMX	670	70.5	4.0	6831	2	A88852	protein unc-22 (im
598	4.0	570	2	T11647	671	70.5	4.0	6839	2	S57242	twitchin (similari
599	4.0	609	2	H82039	672	70.5	4.0	7160	2	T27935	hypothetical prote
600	4.0	615	2	S38575	673	70	4.0	115	1	KWMSL6	IG kappa chain pre
601	4.0	682	2	T22064	674	70	4.0	203	2	S23043	T-cell receptor ga
602	4.0	687	2	A49636	675	70	4.0	224	2	T37243	CMAR-35 antigen -
603	4.0	690	2	A24545	676	70	4.0	236	2	S25746	IG lambda chain -
604	4.0	691	2	B89797	677	70	4.0	283	2	AB0105	probable maltodext
605	4.0	765	2	E96558	678	70	4.0	292	2	T44230	hypothetical prote
606	4.0	821	1	TVHP2	679	70	4.0	299	2	D83010	probable binding p
607	4.0	876	2	T51507	680	70	4.0	304	2	G71624	hypothetical prote
608	4.0	902	1	S54595	681	70	4.0	347	2	T29415	hypothetical prote
609	4.0	940	2	T41992	682	70	4.0	356	2	G82938	hemim transport sy
610	4.0	956	2	G70327	683	70	4.0	374	2	A46352	ORF1 protein - Chl
611	4.0	1018	2	A54744	684	70	4.0	403	2	B36151	tryptophan synthas
612	4.0	1027	2	B55089	685	70	4.0	410	2	I50494	serine proteinase
613	4.0	1082	2	S64903	686	70	4.0	469	2	T46929	hypothetical prote

687	70	4.0	491	2	T27661	hypothetical prote	760	69.5	3.9	1045	2	G69167	cobalamin biosynth
688	70	4.0	517	2	T00980	hypothetical prote	761	69.5	3.9	1102	2	T28666	protein kinase C-r
689	70	4.0	536	2	T37544	hypothetical serin	762	69.5	3.9	1172	2	F70535	probable ppoB prot
690	70	4.0	548	2	B71549	hypothetical prote	763	69.5	3.9	1199	2	C71500	probable swi/anf h
691	70	4.0	550	2	T03714	s-epi-aristolochin	764	69.5	3.9	1260	1	S05479	neural cell adhesi
692	70	4.0	576	2	A36604	interleukin-1 rece	765	69.5	3.9	1463	2	T30290	AAS surface protei
693	70	4.0	599	2	T48450	hypothetical prote	766	69.5	3.9	1832	2	AC2594	glutamate synthase
694	70	4.0	609	2	AE2062	gamma-glutamyltran	767	69.5	3.9	1858	2	D97376	hypothetical prote
695	70	4.0	611	1	W1WLEP	E1 protein - Europ	768	69	3.9	115	2	C90907	hypothetical prote
696	70	4.0	611	2	H70938	probable fadEs pro	769	69	3.9	139	2	AH1847	photosystem I reac
697	70	4.0	648	2	T08856	hypothetical prote	770	69	3.9	222	2	A69458	conserved hypothet
698	70	4.0	687	1	A35045	protein-glutamine	771	69	3.9	279	2	S04693	T-cell receptor de
699	70	4.0	790	2	T01537	S-receptor kinase	772	69	3.9	289	2	T18048	hypothetical prote
700	70	4.0	805	2	S68441	leptin receptor, s	773	69	3.9	291	2	A87153	carbohydrate degra
701	70	4.0	810	1	S57196	calpain (EC 3.4.22	774	69	3.9	306	2	T25625	hypothetical prote
702	70	4.0	818	2	T32154	hypothetical prote	775	69	3.9	330	2	AD1533	hypothetical prote
703	70	4.0	828	2	AD2004	hypothetical prote	776	69	3.9	348	2	D96815	probable gamma-glu
704	70	4.0	837	2	A34898	granulocyte colony	777	69	3.9	363	2	AG0675	probable secreted
705	70	4.0	838	2	AC1064	outer membrane fim	778	69	3.9	390	2	F72863	AcMPV orf109 - Bo
706	70	4.0	849	2	T22306	hypothetical prote	779	69	3.9	391	2	T41849	ACMPV orf109 - Bo
707	70	4.0	892	2	S68439	leptin receptor, s	780	69	3.9	396	2	T36678	probable septum si
708	70	4.0	894	2	S68437	leptin receptor, s	781	69	3.9	418	2	T35753	probable periplasm
709	70	4.0	900	2	S68440	leptin receptor, s	782	69	3.9	428	2	S09134	Gene ND4L intron 1
710	70	4.0	933	2	H90247	ATP-dependent heli	783	69	3.9	461	2	F83772	hypothetical prote
711	70	4.0	990	2	T16554	hypothetical prote	784	69	3.9	465	2	B85358	SERINE CARBOXYPEP
712	70	4.0	1040	2	A34695	axonal glycoprotei	785	69	3.9	469	2	T46930	hypothetical prote
713	70	4.0	1086	2	T40354	hypothetical prote	786	69	3.9	490	2	B28516	cytochrome P450 2C
714	70	4.0	1092	2	T30214	fibrinogen-binding	787	69	3.9	493	2	E71008	hypothetical prote
715	70	4.0	1162	2	S68438	leptin receptor, s	788	69	3.9	501	1	FWLBE2	Li protein - bovin
716	70	4.0	1190	2	T00842	probable histidine	789	69	3.9	505	1	FWICA	H+-transporting tw
717	70	4.0	1317	2	T41950	retrovirus-related	790	69	3.9	542	2	T20457	hypothetical prote
718	70	4.0	1456	1	WMGPGV	RNA-directed RNA p	791	69	3.9	584	1	ALBY	alpha-glucosidase
719	70	4.0	1456	2	JO2294	hypothetical 165.1	792	69	3.9	615	2	JE0358	ra1b binding prote
720	70	4.0	2004	2	AC0314	probable membrane	793	69	3.9	633	2	D82527	proteinase IV XP26
721	70	4.0	2183	2	T42764	coagulation factor	794	69	3.9	644	2	A25684	hypothetical prote
722	70	4.0	4199	2	S76412	hypothetical prote	795	69	3.9	653	2	A54366	sodium/phosphate c
723	69.5	3.9	219	2	S74483	hypothetical prote	796	69	3.9	657	2	S25184	cepi protein - Cor
724	69.5	3.9	285	1	I38548	alcohol sulfotrans	797	69	3.9	715	2	I45832	scinderin - bovine
725	69.5	3.9	332	2	E71105	hypothetical prote	798	69	3.9	715	2	T10049	adseverin - mouse
726	69.5	3.9	338	1	DENSM	malate dehydrogena	799	69	3.9	773	2	T46283	hypothetical prote
727	69.5	3.9	346	2	T49148	nitrilase (EC 3.5.	800	69	3.9	824	2	T51057	related to tol pro
728	69.5	3.9	366	2	E97304	iron-regulated ABC	801	69	3.9	919	2	C86578	YopC/gen secretion
729	69.5	3.9	407	2	T07732	hypothetical prote	802	69	3.9	919	2	F72045	type III secretion
730	69.5	3.9	427	2	C23703	ribulose-bisphosph	803	69	3.9	1049	2	S67613	vacuolar carboxype
731	69.5	3.9	432	2	D70353	adenylosuccinate 1	804	69	3.9	1052	2	A82127	ribonuclease E VC2
732	69.5	3.9	437	2	H86144	hypothetical prote	805	69	3.9	1244	2	T19615	hypothetical prote
733	69.5	3.9	444	2	F97750	tolB protein precu	806	69	3.9	1283	2	T39174	hypothetical Serin
734	69.5	3.9	447	2	B81519	UDP-N-acetylmuramo	807	69	3.9	1357	2	S61187	probable membrane
735	69.5	3.9	447	2	A86603	muramoyl-DAP ligas	808	69	3.9	1360	2	T32833	hypothetical prote
736	69.5	3.9	447	2	F72021	protein lin-42 [im	809	69	3.9	1442	2	T18538	patched protein -
737	69.5	3.9	453	2	B88040	hypothetical prote	810	69	3.9	1656	2	S54520	probable membrane
738	69.5	3.9	461	2	T47782	probable membrane	811	69	3.9	1802	2	S52611	TyB protein - Yeas
739	69.5	3.9	503	2	S63257	fatty acid elongas	812	69	3.9	2132	1	A55182	aggreacan precursor
740	69.5	3.9	506	2	T05272	protein-tyrosine k	813	69	3.9	2437	2	T18482	hypothetical prote
741	69.5	3.9	523	1	TVFVMT	amds protein - Eme	814	69	3.9	4563	1	LPHUB	apolipoprotein B-1
742	69.5	3.9	548	2	A26511	transcription fact	815	69	3.9	5188	2	B85547	probable RTX famil
743	69.5	3.9	548	2	S27958	conserved hypothet	816	69	3.9	5291	2	F90696	hypothetical prote
744	69.5	3.9	568	2	T39840	delayed rectifier	817	69	3.9	10797	2	T30192	probable peptide s
745	69.5	3.9	585	2	A39395	conserved hypothet	818	68.5	3.9	134	2	S11245	Ig kappa chain pre
746	69.5	3.9	616	2	D64569	amino acid transpo	819	68.5	3.9	135	2	JU0472	T-cell receptor be
747	69.5	3.9	633	2	S19352	dnak-type molecula	820	68.5	3.9	145	2	S36324	T-cell receptor de
748	69.5	3.9	640	2	T43724	hypothetical prote	821	68.5	3.9	227	2	T33766	hypothetical prote
749	69.5	3.9	682	2	D90946	hypothetical prote	822	68.5	3.9	228	2	A32200	two-component resp
750	69.5	3.9	682	2	H85794	carboxy-terminal p	823	68.5	3.9	234	2	S25757	Ig lambda chain -
751	69.5	3.9	682	2	A41798	hepatocyte growth	824	68.5	3.9	234	2	S14237	Ig kappa chain pre
752	69.5	3.9	710	1	I51283	pombe specific hyp	825	68.5	3.9	240	2	A39016	T-cell surface gly
753	69.5	3.9	736	2	T40904	hypothetical prote	826	68.5	3.9	267	2	G90579	hypothetical prote
754	69.5	3.9	752	2	T24266	genome polyprotein	827	68.5	3.9	268	2	S48942	hypothetical prote
755	69.5	3.9	776	2	A41704	probable sugar tra	828	68.5	3.9	292	2	C64699	proteinase IV (EC
756	69.5	3.9	776	2	F81289	hypothetical prote	829	68.5	3.9	296	2	G65002	hypothetical prote
757	69.5	3.9	846	1	T04533	hypothetical prote	830	68.5	3.9	299	2	T32094	hypothetical prote
758	69.5	3.9	849	1	UYFVAD	noncapsid protein	831	68.5	3.9	310	2	A41776	syndecan 1 precurs
759	69.5	3.9	1034	2	H86399	protein F17L21.26	832	68.5	3.9	327	2	A81192	replication protei

833	68.5	3.9	328	2	I47161	Ig gamma 3 chain c	906	68	3.8	401	2	B89863	argininosuccinate
834	68.5	3.9	329	2	T19872	hypothetical prote	907	68	3.8	409	1	PAWTF	fructose-bisphosph
835	68.5	3.9	356	2	A70852	hypothetical prote	908	68	3.8	412	2	T35664	probable prokaryot
836	68.5	3.9	375	2	E98667	hypothetical prote	909	68	3.8	431	2	F64072	multidrug resistan
837	68.5	3.9	393	2	B48965	subtilin biosynthe	910	68	3.8	434	2	D87296	hypothetical prote
838	68.5	3.9	423	2	AG0451	maltooporin [import	911	68	3.8	444	2	S76138	hypothetical prote
839	68.5	3.9	448	2	G69960	exodeoxyribonuclea	912	68	3.8	459	2	T21105	hypothetical prote
840	68.5	3.9	458	1	RWHUT4	T-cell surface gly	913	68	3.8	466	2	T46054	hypothetical prote
841	68.5	3.9	463	2	T19343	hypothetical prote	914	68	3.8	471	2	A81680	conserved hypotet
842	68.5	3.9	464	2	T06176	ribulose-bisphosph	915	68	3.8	479	1	S22542	transcription fact
843	68.5	3.9	493	2	T41397	DNA damage inducib	916	68	3.8	526	1	P5XR10	outer capsid prote
844	68.5	3.9	498	2	QJ2353	glycoprotein E pre	917	68	3.8	528	2	T38027	hypothetical prote
845	68.5	3.9	513	2	H90401	flagella-related p	918	68	3.8	541	2	E95789	protein T23E18.10
846	68.5	3.9	542	2	S30884	SRP1 protein - yea	919	68	3.8	584	2	S46183	alpha-glucosidase
847	68.5	3.9	555	2	F70372	dihydroxyacid dehy	920	68	3.8	602	2	D90557	hypothetical prote
848	68.5	3.9	561	2	S63388	probable membrane	921	68	3.8	632	2	T37810	RNA-binding post-t
849	68.5	3.9	561	2	A59182	protein-tyrosine k	922	68	3.8	637	2	D82816	fimbrial assembly
850	68.5	3.9	581	2	T10178	aldehyde-ferredoxi	923	68	3.8	638	2	S54418	fibronectin-bindin
851	68.5	3.9	589	2	T40252	hypothetical prote	924	68	3.8	640	2	S35734	DNA topoisomerase
852	68.5	3.9	592	2	S54489	phosphoribosylamin	925	68	3.8	645	2	E96631	probable receptor
853	68.5	3.9	601	2	AD1250	DNA mismatch repai	926	68	3.8	649	1	CZCLDM	cellulase (EC 3.2.
854	68.5	3.9	606	2	AP2303	GTP-binding tyrosi	927	68	3.8	656	2	F71675	hypothetical prote
855	68.5	3.9	606	2	H97678	hypothetical prote	928	68	3.8	690	2	JC4185	GGD5F family prote
856	68.5	3.9	630	2	S77346	hypothetical prote	929	68	3.8	710	2	F82492	hypothetical prote
857	68.5	3.9	636	2	A86248	protein T23J18.9 [	930	68	3.8	721	2	T27570	androgen-regulated
858	68.5	3.9	654	2	A96556	methyl-accepting c	931	68	3.8	789	2	S28259	cadherin 8 - human
859	68.5	3.9	672	2	D81746	type III secretion	932	68	3.8	793	2	D38992	hypothetical prote
860	68.5	3.9	689	2	S70661	transferrin-bindin	933	68	3.8	795	2	T21487	coatomer complex b
861	68.5	3.9	772	1	T05753	S-receptor kinase	934	68	3.8	814	1	C40618	fimbrial outer mem
862	68.5	3.9	776	2	B41704	genome polyprotein	935	68	3.8	878	2	AH2075	ferrichrome-iron r
863	68.5	3.9	789	2	S62172	SHE4 protein - yea	936	68	3.8	896	2	S26984	probable DNA-direc
864	68.5	3.9	818	2	B83537	hypothetical prote	937	68	3.8	901	2	JB0062	core protein VP3 -
865	68.5	3.9	827	2	A37849	S-layer protein -	938	68	3.8	906	1	IXLX2	N-cadherin 2 precu
866	68.5	3.9	831	2	JQ1655	prolactin receptor	939	68	3.8	912	2	AS4423	brevican precursor
867	68.5	3.9	906	1	IJHUCN	cadherin 2 precurs	940	68	3.8	940	2	AB1744	internalin protein
868	68.5	3.9	950	2	T11134	ionotropic glutama	941	68	3.8	962	2	S03818	carboxymethylcellu
869	68.5	3.9	972	1	TVHUMD	macrophage colony-	942	68	3.8	963	2	AS7238	iron-responsive el
870	68.5	3.9	976	2	A42466	alpha-amylase (EC	943	68	3.8	997	2	D88473	protein F40H6.2 [1
871	68.5	3.9	1043	2	A56037	DNA-binding protei	944	68	3.8	1019	2	T13039	tyrosine kinase re
872	68.5	3.9	1074	2	F72212	conserved hypotet	945	68	3.8	1071	2	T52306	methionine S-methy
873	68.5	3.9	1086	2	T12894	Ca2+-transporting	946	68	3.8	1147	2	S64930	serine/threonine-s
874	68.5	3.9	1134	2	S53955	hypothetical prote	947	68	3.8	1174	2	I38140	protein-tyrosine-p
875	68.5	3.9	1257	1	A41060	neural cell adhesi	948	68	3.8	1192	2	F88062	protein ZK250.10 [
876	68.5	3.9	1269	2	A90267	proteinase related	949	68	3.8	1195	2	S61886	chitin synthase [E
877	68.5	3.9	1466	2	A64426	SP42 protein - yea	950	68	3.8	1281	2	I48123	p-glycoprotein iso
878	68.5	3.9	1520	2	A81731	polymorphic membra	951	68	3.8	1282	2	JC4393	microbial collagen
879	68.5	3.9	1767	2	T20766	hypothetical prote	952	68	3.8	1291	2	T21694	hypothetical prote
880	68.5	3.9	2013	2	A11489	probable peptidogl	953	68	3.8	1295	2	T30528	reverse transcript
881	68.5	3.9	2288	2	T30568	acetyl-CoA carboxy	954	68	3.8	1318	2	T05745	hypothetical prote
882	68.5	3.9	3229	2	S27852	probable cell-surf	955	68	3.8	1458	2	A45665	adult-specific bru
883	68.5	3.9	4116	2	T13719	calo protein - fru	956	68	3.8	1466	2	T32422	hypothetical prote
884	68	3.8	142	2	S36307	T-cell receptor de	957	68	3.8	1664	2	H82601	conserved hypotet
885	68	3.8	144	2	A11529	mannose-specific p	958	68	3.8	1707	2	T18951	hypothetical prote
886	68	3.8	155	2	I64130	PAL cross-reacting	959	68	3.8	1786	1	H71527	probable exinucle
887	68	3.8	157	2	T09659	pathogenesis-relat	960	68	3.8	1946	2	AE1449	hypothetical prote
888	68	3.8	180	2	A71634	hypothetical prote	961	68	3.8	2124	2	A28452	hypothetical prote
889	68	3.8	221	2	S73349	adhesin PI precurs	962	68	3.8	221	1	B42521	hypothetical prote
890	68	3.8	231	2	D64461	hypothetical prote	963	68	3.8	229	2	A20969	ig kappa chain pre
891	68	3.8	233	2	H95345	NapC membrane prot	964	67.5	3.8	261	2	S55199	hypothetical prote
892	68	3.8	266	2	G69483	hypothetical prote	965	67.5	3.8	267	2	I72882	FC gamma receptor
893	68	3.8	275	2	S03967	intercellular adhe	966	67.5	3.8	277	2	E97703	hypothetical prote
894	68	3.8	276	2	D82169	conserved hypotet	967	67.5	3.8	278	2	JC1507	biliary glycoprote
895	68	3.8	286	2	A82159	hypothetical prote	968	67.5	3.8	299	2	F82975	hypothetical prote
896	68	3.8	311	2	AH3197	transmembrane sens	969	67.5	3.8	315	2	G69785	mannose-6-phosphat
897	68	3.8	326	2	T51811	protein farnesyltr	970	67.5	3.8	327	2	T22407	hypothetical prote
898	68	3.8	330	2	B96027	probable aliphatic	971	67.5	3.8	329	1	G2GP	ig gamma-2 chain C
899	68	3.8	338	2	C83653	oligopeptide ABC t	972	67.5	3.8	345	2	I58406	LEK2 - rat
900	68	3.8	340	2	T49006	farnesyltransferas	973	67.5	3.8	348	1	MMNHPB	outer membrane pro
901	68	3.8	341	2	AE1824	permease protein o	974	67.5	3.8				
902	68	3.8	355	2	S58401	synaptotagmin VIII	975	67.5	3.8				
903	68	3.8	371	2	E71378	probable DNA polym	976	67.5	3.8				
904	68	3.8	378	2	E84806	probable elongatio	977	67.5	3.8				
905	68	3.8	385	2	T27626	hypothetical prote	978	67.5	3.8				

979	67.5	3.8	348	2	B70743	hypothetical prote	1052	67	3.8	127	2	S52447	Ig kappa chain V r
980	67.5	3.8	357	2	T34012	hypothetical prote	1053	67	3.8	128	2	S31488	Ig kappa chain pre
981	67.5	3.8	360	2	T27022	hypothetical prote	1054	67	3.8	131	2	E30552	T-cell activation
982	67.5	3.8	361	2	D83798	phosphoserine amin	1055	67	3.8	135	2	S49200	cytochrome b5 - co
983	67.5	3.8	362	2	A81397	conserved hypothet	1056	67	3.8	175	2	B70221	rev protein (rev)
984	67.5	3.8	364	2	T46630	cysteine proteinas	1057	67	3.8	182	2	T23259	hypothetical prote
985	67.5	3.8	364	2	T12039	cysteine proteinas	1058	67	3.8	214	2	B71169	probable flagellin
986	67.5	3.8	367	2	AF2494	hypothetical prote	1059	67	3.8	239	2	AC2042	hypothetical prote
987	67.5	3.8	370	2	S29139	aggreccan - pig (fr	1060	67	3.8	255	2	F69962	amino acid ABC tra
988	67.5	3.8	402	2	T25732	hypothetical prote	1061	67	3.8	282	2	B84984	geranyltransferas
989	67.5	3.8	426	2	I36948	IG epsilon-chain -	1062	67	3.8	300	2	H64050	glucose kinase hom
990	67.5	3.8	443	2	T19512	hypothetical prote	1063	67	3.8	302	2	AC1387	phosphate ABC tran
991	67.5	3.8	450	2	H71135	probable adenylosu	1064	67	3.8	302	2	AE1762	phosphate ABC tran
992	67.5	3.8	451	2	T06090	hypothetical prote	1065	67	3.8	311	2	C86638	glycosyl transfera
993	67.5	3.8	458	2	A83095	UDP-N-acetylmuram	1066	67	3.8	358	2	G64461	biotin synthase (E
994	67.5	3.8	466	2	A11894	two-component sens	1067	67	3.8	373	1	PDBVB	Rp1 protein - yea
995	67.5	3.8	487	2	S65133	butyrophilin - mou	1068	67	3.8	430	2	T14420	S-locus-specific g
996	67.5	3.8	510	2	A87482	conserved hypothet	1069	67	3.8	441	2	F71425	hypothetical prote
997	67.5	3.8	511	2	A46020	potassium channel	1070	67	3.8	450	2	S38424	S-locus-specific g
998	67.5	3.8	511	2	S07095	59K antigen - Chla	1071	67	3.8	461	2	T09933	probable phosphodi
999	67.5	3.8	525	2	JQ0642	hypothetical prote	1072	67	3.8	474	2	I50830	Ig mu chain - Lepi
1000	67.5	3.8	527	2	G85760	hypothetical prote	1073	67	3.8	477	2	G86833	6-phospho-beta-glu
1001	67.5	3.8	527	2	H90858	hypothetical prote	1074	67	3.8	495	1	A26396	T-cell surface gly
1002	67.5	3.8	541	1	A43610	protein-tyrosine k	1075	67	3.8	518	2	JC4024	poliovirus recepto
1003	67.5	3.8	542	1	TVHUSC	protein-tyrosine k	1076	67	3.8	524	2	G64243	hypothetical prote
1004	67.5	3.8	547	2	B45808	B-lymphocyte antig	1077	67	3.8	532	2	C97228	probable peptide A
1005	67.5	3.8	547	2	T27253	hypothetical prote	1078	67	3.8	542	2	T41650	importin alpha sub
1006	67.5	3.8	567	2	S29498	lymphocyte antigen	1079	67	3.8	544	2	S41626	spike protein chai
1007	67.5	3.8	570	2	A11828	flavoprotein limpo	1080	67	3.8	569	2	S64957	asperillopepsin I
1008	67.5	3.8	572	2	S55982	asparagine synthas	1081	67	3.8	599	2	S55363	maltase-like prote
1009	67.5	3.8	584	2	S48327	hypothetical prote	1082	67	3.8	619	2	S67067	probable membrane
1010	67.5	3.8	591	2	S73708	MG321 homolog H08	1083	67	3.8	622	2	H64447	hypothetical prote
1011	67.5	3.8	619	2	A13336	potassium/proton a	1084	67	3.8	623	2	A64774	glucokinase regula
1012	67.5	3.8	621	2	A72091	metalloproteinase	1085	67	3.8	625	1	S52485	ybaU protein - Esc
1013	67.5	3.8	621	2	D81578	zinc proteinase Cp	1086	67	3.8	661	1	G71063	probable ferrous i
1014	67.5	3.8	627	2	D69556	ntic family transc	1087	67	3.8	690	2	H71237	hypothetical prote
1015	67.5	3.8	651	2	T49986	lectin-like protei	1088	67	3.8	717	2	T25431	hypothetical prote
1016	67.5	3.8	697	2	E95196	neuraminidase B (i	1089	67	3.8	721	2	A12447	hypothetical prote
1017	67.5	3.8	726	2	AG0837	TouB-dependent out	1090	67	3.8	746	2	A75018	transport protein
1018	67.5	3.8	732	1	JU0132	acylaminoacyl-pept	1091	67	3.8	747	2	T23607	hypothetical prote
1019	67.5	3.8	748	2	I48744	semaphorin A - mou	1092	67	3.8	750	2	T19080	hypothetical prote
1020	67.5	3.8	759	2	S67164	probable membrane	1093	67	3.8	836	2	B84417	cell surface glyco
1021	67.5	3.8	776	2	S67053	probable membrane	1094	67	3.8	850	2	AF3484	hypothetical trans
1022	67.5	3.8	790	2	G02678	cadherin-14 - huma	1095	67	3.8	852	2	A28459	cell surface glyco
1023	67.5	3.8	790	2	A39627	protein-tyrosine k	1096	67	3.8	871	2	G86586	DNA topoisomerase
1024	67.5	3.8	832	2	AD1096	internalin protein	1097	67	3.8	871	2	D72038	DNA topoisomerase
1025	67.5	3.8	837	2	B85583	protein K07E3.2 (i	1098	67	3.8	875	2	S62177	HfR2 protein - yea
1026	67.5	3.8	855	2	T10665	hypothetical prote	1099	67	3.8	876	2	I49152	protein-tyrosine k
1027	67.5	3.8	866	2	T10587	serine/threonine-s	1100	67	3.8	898	2	T49492	hypothetical prote
1028	67.5	3.8	879	2	S73757	hypothetical prote	1101	67	3.8	920	2	JC7313	aryl hydrocarbon r
1029	67.5	3.8	906	2	AG1957	hypothetical prote	1102	67	3.8	939	2	AE2275	hypothetical prote
1030	67.5	3.8	926	2	D86897	hypothetical prote	1103	67	3.8	974	2	B86613	zinc metalloprotei
1031	67.5	3.8	933	2	AD3309	hypothetical membr	1104	67	3.8	974	2	T29545	hypothetical prote
1032	67.5	3.8	944	2	T47246	chitin synthase (E	1105	67	3.8	976	2	T29583	hypothetical prote
1033	67.5	3.8	956	2	JH0826	glutamate ionotrop	1106	67	3.8	980	2	I57936	glutamate receptor
1034	67.5	3.8	992	2	QJ0165	Env protein - Maed	1107	67	3.8	981	2	T18234	beta transducin ho
1035	67.5	3.8	1036	2	A29832	HPI layer surface	1108	67	3.8	1040	2	D81379	transmembrane effl
1036	67.5	3.8	1042	2	E85968	evolved beta-D-gal	1109	67	3.8	1048	2	H64459	hypothetical prote
1037	67.5	3.8	1042	2	F91123	conserved hypothet	1110	67	3.8	1070	2	JC4593	protein-tyrosine k
1038	67.5	3.8	1061	2	D98008	hypothetical prote	1111	67	3.8	1115	1	IUMSNL	neural cell adhesi
1039	67.5	3.8	1118	2	T27865	probable pyrolysin	1112	67	3.8	1134	2	T04587	hypothetical prote
1040	67.5	3.8	1155	2	H71456	chitinase A (impor	1113	67	3.8	1151	2	AG1717	probable peptidogl
1041	67.5	3.8	1215	2	T43916	chitinase A (impor	1114	67	3.8	1170	1	TSHUPL	thrombospondin 1 p
1042	67.5	3.8	1229	2	D85023	P-glycoprotein-lik	1115	67	3.8	1264	2	S41603	type V adenylyl cy
1043	67.5	3.8	1229	2	T52319	protein-tyrosine-lik	1116	67	3.8	1309	1	BVBVD9	RAD9 protein - yea
1044	67.5	3.8	1260	1	TVRTNU	protein-tyrosine k	1117	67	3.8	1328	2	T23007	hypothetical prote
1045	67.5	3.8	1263	2	T13465	hypothetical prote	1118	67	3.8	1365	2	T45031	hypothetical prote
1046	67.5	3.8	1330	2	S49010	embryonic receptor	1119	67	3.8	1428	2	S62419	hypothetical prote
1047	67.5	3.8	1471	2	T40117	myosin-2 isoform -	1120	67	3.8	1441	2	T13717	CRAG protein - fru
1048	67.5	3.8	1928	2	J50610	beta-galactosidase	1121	67	3.8	1445	1	A48148	protein-tyrosine-p
1049	67.5	3.8	2338	2	I73957	kinase-related pro	1122	67	3.8	1533	2	F71274	hypothetical prote
1050	67.5	3.8	3026	3	T28431	variant surface pr	1123	67	3.8	1589	2	T22668	hypothetical prote
1051	67.5	3.8	4660	2	T42737	gp330 protein prec	1124	67	3.8	1680	2	T41628	probable transcrip



1125	67	3.8	1723	2	H86557	polymorphic membra	1198	66.5	3.8	1117	2	JC4934	delta-crystallin/S
1126	67	3.8	1723	2	E72067	polymorphic membra	1199	66.5	3.8	1160	2	T39898	carbamoyl-phosphat
1127	67	3.8	1732	2	C81601	polymorphic membra	1200	66.5	3.8	1181	2	T20386	hypothetical prote
1128	67	3.8	1742	2	S24600	projectin - fruit	1201	66.5	3.8	1182	2	S59951	DNA-polymerase RNA p
1129	67	3.8	1790	1	S27772	vitellogenin precu	1202	66.5	3.8	1183	2	H89821	RNA polymerase bet
1130	67	3.8	1813	2	T30564	resistance protein	1203	66.5	3.8	1184	2	A42904	adenylcyclase ty
1131	67	3.8	2095	2	S29529	genome polyprotein	1204	66.5	3.8	1344	2	T14316	rig-1 protein - mo
1132	67	3.8	2380	2	T29551	hypothetical prote	1205	66.5	3.8	1376	2	F83711	exopolysaccharona
1133	67	3.8	2626	2	T31099	myosin-RhocAP prot	1206	66.5	3.8	1447	2	A54100	tumor suppressor p
1134	66.5	3.8	136	2	C72524	hypothetical prote	1207	66.5	3.8	1462	2	T06819	DNA topoisomerase
1135	66.5	3.8	147	2	JC7237	receptor-activity-	1208	66.5	3.8	1471	2	F86218	protein F22013.8 [
1136	66.5	3.8	181	2	AC0686	hypothetical prote	1209	66.5	3.8	1484	2	T42632	breast cancer tumo
1137	66.5	3.8	191	2	AH0196	probable lipoprote	1210	66.5	3.8	1545	2	T26589	hypothetical prote
1138	66.5	3.8	218	2	D72494	probable thiosulfa	1211	66.5	3.8	1565	2	T01060	hypothetical prote
1139	66.5	3.8	228	2	AG2107	hypothetical prote	1212	66.5	3.8	1616	2	T00713	helicase homolog F
1140	66.5	3.8	245	2	T12334	L-ascorbate peroxi	1213	66.5	3.8	1643	2	T14274	versican precursor
1141	66.5	3.8	245	2	H71429	hypothetical prote	1214	66.5	3.8	2089	2	C85426	ATM-like protein [
1142	66.5	3.8	250	2	S64849	hypothetical prote	1215	66.5	3.8	2303	1	GNNYTM	genome polyprotein
1143	66.5	3.8	285	2	T12156	nodulin, isoform N	1216	66.5	3.8	2470	2	I50726	cation-independent
1144	66.5	3.8	301	2	S57531	transcription regu	1217	66.5	3.8	2588	2	AI2136	peptide synthetase
1145	66.5	3.8	318	2	S61840	porin class PIB -	1218	66.5	3.8	3262	2	AH2137	hypothetical prote
1146	66.5	3.8	328	2	D69452	conserved hypothet	1219	66.5	3.8	3305	2	T18358	apolipoprotein prec
1147	66.5	3.8	335	2	A53434	cell surface glyco	1220	66.5	3.8	3381	2	T42389	versican precursor
1148	66.5	3.8	344	2	I51330	androgen receptor	1221	66.5	3.8	3738	2	T05501	hypothetical prote
1149	66.5	3.8	352	2	T09760	chymopain (EC 3.	1222	66.5	3.8	4092	1	S38128	dysmin heavy chain
1150	66.5	3.8	358	2	G70026	conserved hypothet	1223	66.5	3.8	4436	2	E71086	hypothetical prote
1151	66.5	3.8	362	2	T41842	AcMNPV orf101 - Bo	1224	66.5	3.8	4447	2	A63679	polyketide synthas
1152	66.5	3.8	367	2	T06529	cysteine proteinas	1225	66.5	3.8	5147	1	IJFFTM	cadherin-related t
1153	66.5	3.8	382	2	C86321	hypothetical prote	1226	66	3.7	118	2	S12627	Ig lambda chain pr
1154	66.5	3.8	384	2	F84675	hypothetical prote	1227	66	3.7	132	1	RWMS12	T-cell receptor ga
1155	66.5	3.8	394	2	AC3364	glutaryl-CoA dehyd	1228	66	3.7	134	2	T52469	cytochrome b5 (imp
1156	66.5	3.8	397	2	T34441	hypothetical prote	1229	66	3.7	167	2	S23579	Ig light chain - r
1157	66.5	3.8	404	1	I61596	advanced glycosyla	1230	66	3.7	182	2	A34647	probable 4-nitroph
1158	66.5	3.8	413	2	H82270	hypothetical prote	1231	66	3.7	189	2	A31348	hypothetical prote
1159	66.5	3.8	417	2	A27775	phosphoglycerate k	1232	66	3.7	192	2	B75144	replication protei
1160	66.5	3.8	422	1	BVBVMS	MSII protein - yea	1233	66	3.7	216	2	S69130	hypothetical prote
1161	66.5	3.8	438	2	A97590	hypothetical prote	1234	66	3.7	226	2	T38234	hypothetical prote
1162	66.5	3.8	438	2	AH2811	ATPase, AAA family	1235	66	3.7	255	2	H72539	probable 4-nitroph
1163	66.5	3.8	438	2	A82262	conserved hypothet	1236	66	3.7	261	2	G87608	hypothetical prote
1164	66.5	3.8	442	2	E65211	chorismate lyase u	1237	66	3.7	272	2	T10116	replication protei
1165	66.5	3.8	453	2	A89873	hypothetical prote	1238	66	3.7	281	2	G71095	hypothetical prote
1166	66.5	3.8	461	2	D96835	probable cyclin, 4	1239	66	3.7	307	2	A71602	S-locus-specific g
1167	66.5	3.8	463	2	T26655	hypothetical prote	1240	66	3.7	324	2	S56435	hypothetical prote
1168	66.5	3.8	475	2	A54879	pregnancy-specific	1241	66	3.7	362	2	T04079	ferredoxin-NADP re
1169	66.5	3.8	491	2	D91217	ketol-acid reducto	1242	66	3.7	376	2	T19186	hypothetical prote
1170	66.5	3.8	491	2	E86063	ketol-acid reducto	1243	66	3.7	381	2	AE2197	ABC transport prot
1171	66.5	3.8	497	2	JB0275	voltage-gated pota	1244	66	3.7	400	2	T24890	hypothetical prote
1172	66.5	3.8	532	2	T15354	hypothetical prote	1245	66	3.7	406	2	H64793	ybdN protein - Eac
1173	66.5	3.8	542	2	A49114	protein-tyrosine k	1246	66	3.7	406	2	A99709	hypothetical prote
1174	66.5	3.8	549	2	H64992	hypothetical prote	1247	66	3.7	406	2	B85559	hypothetical prote
1175	66.5	3.8	553	2	T15220	hypothetical prote	1248	66	3.7	417	1	S22784	acetyl-CoA C-acyl
1176	66.5	3.8	557	2	S21596	extracellular prot	1249	66	3.7	428	2	T14529	S-locus-specific g
1177	66.5	3.8	592	2	S25705	Ig mu chain - shee	1250	66	3.7	432	2	T05236	hypothetical prote
1178	66.5	3.8	616	2	G64160	GTP-binding protei	1251	66	3.7	448	2	G83818	hypothetical prote
1179	66.5	3.8	636	2	H87789	protein C34G6.1 [i	1252	66	3.7	451	2	T30603	perlecan homolog 2
1180	66.5	3.8	656	1	S59631	endo-1,4-beta-xyla	1253	66	3.7	457	2	D69059	glycinamide ribonu
1181	66.5	3.8	679	2	C71007	probable formate d	1254	66	3.7	459	2	T08594	probable sulfate a
1182	66.5	3.8	697	2	B98063	exo-alpha-sialidas	1255	66	3.7	466	2	T27120	hypothetical prote
1183	66.5	3.8	709	2	A33364	carcinoembryonic a	1256	66	3.7	469	2	E70076	arabinan endo-1,5-
1184	66.5	3.8	718	1	VCPVIM	coat protein VP1 -	1257	66	3.7	471	2	S14165	cyclin B1 - yeast
1185	66.5	3.8	773	2	S46011	probable pre-mRNA-	1258	66	3.7	489	1	VGBETA	glycoprotein A - t
1186	66.5	3.8	848	2	C70203	DNA topoisomerase	1259	66	3.7	495	2	C71679	UDP-n-acetylmuram
1187	66.5	3.8	862	2	B36786	hypothetical prote	1260	66	3.7	525	2	S55099	GMP synthase (glut
1188	66.5	3.8	917	2	I48950	telencephalin prec	1261	66	3.7	532	1	A34104	protein-tyrosine k
1189	66.5	3.8	921	2	T51136	ionotropic glutama	1262	66	3.7	532	1	B34104	protein-tyrosine k
1190	66.5	3.8	923	2	T41350	meiotic recombinat	1263	66	3.7	538	2	JC2457	vascular cell adhe
1191	66.5	3.8	969	2	C86394	protein T24P13.14	1264	66	3.7	545	2	D81973	probable integral
1192	66.5	3.8	1005	2	S73711	probable lipoprote	1265	66	3.7	550	2	T37579	DiGeorge syndrome
1193	66.5	3.8	1009	2	JH0266	glutamate receptor	1266	66	3.7	553	2	T48486	hypothetical prote
1194	66.5	3.8	1044	2	T10050	integrin alpha-v c	1267	66	3.7	580	2	H72270	ABC transporter, A
1195	66.5	3.8	1061	2	JC7116	Xsal-3 protein - A	1268	66	3.7	589	2	B90605	hypothetical prote
1196	66.5	3.8	1080	2	A35088	phycobilisome link	1269	66	3.7	592	2	E70455	sulfur oxidation p
1197	66.5	3.8	1097	2	T45622	hypothetical prote	1270	66	3.7	603	2	S03020	dopamine beta-mono

1271 66 3.7 624 2 D84986 heat shock protein  
 1272 66 3.7 631 2 I52257 episialin - mouse  
 1273 66 3.7 640 2 B95784 hypothetical prote  
 1274 66 3.7 662 2 T23271 hypothetical prote  
 1275 66 3.7 687 2 G81970 probable glycine-t  
 1276 66 3.7 719 2 S44237 trypanostigme ac  
 1277 66 3.7 738 2 A40096 platelet-endotheli  
 1278 66 3.7 747 2 S66959 hypothetical prote  
 1279 66 3.7 750 2 T04010 hypothetical prote  
 1280 66 3.7 751 2 T01449 cytoskeletal prote  
 1281 66 3.7 754 2 JC4898 Down-syndrome-crit  
 1282 66 3.7 808 2 D81924 hypothetical prote  
 1283 66 3.7 810 2 A81965 hemeoglobin-haptog  
 1284 66 3.7 815 2 T35970 probable efflux pr  
 1285 66 3.7 833 2 T49782 related to alkalini  
 1286 66 3.7 839 2 T15753 hypothetical prote  
 1287 66 3.7 851 2 T47495 hypothetical prote  
 1288 66 3.7 863 2 AE0525 outer membrane ush  
 1289 66 3.7 864 2 H85335 hypothetical prote  
 1290 66 3.7 864 2 T04518 hypothetical prote  
 1291 66 3.7 901 2 AE0519 preprotein translo  
 1292 66 3.7 902 2 A60560 formyltetrahydrofo  
 1293 66 3.7 912 1 IJCHCN N-cadherin precurs  
 1294 66 3.7 920 2 B84640 probable ligand-ga  
 1295 66 3.7 961 2 G90053 hypothetical prote  
 1296 66 3.7 974 2 A72012 metalloproteinase,  
 1297 66 3.7 977 2 I45877 protein-tyrosine k  
 1298 66 3.7 979 2 JH0589 glutamate receptor  
 1299 66 3.7 979 2 JH0592 glutamate receptor  
 1300 66 3.7 1006 2 AD2195 hypothetical prote  
 1301 66 3.7 1043 2 T15191 hypothetical prote  
 1302 66 3.7 1053 2 S72194 hydroxymethylgluta  
 1303 66 3.7 1065 2 H95321 NOLG efflux transp  
 1304 66 3.7 1100 2 A35007 ATP citrate (pro-S  
 1305 66 3.7 1105 2 S21173 ATP citrate (pro-S  
 1306 66 3.7 1112 2 T30202 probable chitin sy  
 1307 66 3.7 1118 2 S44641 hypothetical prote  
 1308 66 3.7 1139 2 T22811 Lin-25 protein - C  
 1309 66 3.7 1207 2 T52459 sensory transducti  
 1310 66 3.7 1223 2 S29717 adenylate cyclase  
 1311 66 3.7 1232 2 T34027 neural cell adhesi  
 1312 66 3.7 1242 2 T39453 probable mrna stab  
 1313 66 3.7 1248 2 C89874 autolysin [impor  
 1314 66 3.7 1335 2 T30211 autolysin E - Stap  
 1315 66 3.7 1353 2 T26301 hypothetical prote  
 1316 66 3.7 1363 2 S44241 surface protein -  
 1317 66 3.7 1367 2 A41228 protein-tyrosine k  
 1318 66 3.7 1349 2 D86338 protein F5W15.18 [  
 1319 66 3.7 1601 2 T18800 hypothetical prote  
 1320 66 3.7 1750 2 G84649 hypothetical prote  
 1321 66 3.7 1792 2 T08878 supervillin P205 -  
 1322 66 3.7 1822 2 T14106 probable GTPase-ac  
 1323 66 3.7 1828 2 T41455 cutl protein - fis  
 1324 66 3.7 1993 2 T30902 sodium channel SC  
 1325 66 3.7 2035 2 AC0233 yersiniabactin bio  
 1326 66 3.7 2041 2 T17439 peptide synthetase  
 1327 66 3.7 2186 2 H89960 hypothetical prote  
 1328 66 3.7 2347 1 TVHURS kinase-related pro  
 1329 66 3.7 2352 2 T30201 Notch homolog prot  
 1330 66 3.7 3415 2 A46105 polyprotein(NS1, N  
 1331 66 3.7 13055 2 T16580 hypothetical prote  
 1332 65.5 3.7 98 1 JG806A cytochrome-c oxida  
 1333 65.5 3.7 105 2 QN0032 early protein gp12  
 1334 65.5 3.7 130 2 S17719 H+-transporting tw  
 1335 65.5 3.7 134 1 RWRBAY T-cell receptor al  
 1336 65.5 3.7 166 2 S04934 T-cell receptor de  
 1337 65.5 3.7 178 1 H81285 probable flagellar  
 1338 65.5 3.7 186 1 Q0BEC6 HQLP1 precursor -  
 1339 65.5 3.7 194 2 T29925 hypothetical prote  
 1340 65.5 3.7 198 2 JCS626 STAR induced STAR  
 1341 65.5 3.7 198 2 JCS760 cytokine-inducible  
 1342 65.5 3.7 200 2 E96912 adenylylsulfate ki  
 1343 65.5 3.7 223 2 A36462 probable transmemb

1344 65.5 3.7 1344 conserved hypothet  
 1345 65.5 3.7 1345 coat protein - tob  
 1346 65.5 3.7 1346 conserved hypothet  
 1347 65.5 3.7 1347 hypothetical prote  
 1348 65.5 3.7 1348 heat shock protein  
 1349 65.5 3.7 1349 UDP-N-acetylenolpy  
 1350 65.5 3.7 1350 concanavalin A pre  
 1351 65.5 3.7 1351 rificin PFB0065w - m  
 1352 65.5 3.7 1352 sporulation protei  
 1353 65.5 3.7 1353 conserved hypothet  
 1354 65.5 3.7 1354 probable chemotaxi  
 1355 65.5 3.7 1355 probable oligopept  
 1356 65.5 3.7 1356 iron(III) dicitrat  
 1357 65.5 3.7 1357 Fit-1S protein pre  
 1358 65.5 3.7 1358 probable binding p  
 1359 65.5 3.7 1359 formate dehydrogen  
 1360 65.5 3.7 1360 hypothetical 39-2K  
 1361 65.5 3.7 1361 hypothetical prote  
 1362 65.5 3.7 1362 hypothetical prote  
 1363 65.5 3.7 1363 hypothetical prote  
 1364 65.5 3.7 1364 glutaryl-CoA dehyd  
 1365 65.5 3.7 1365 Ig gamma-3 chain C  
 1366 65.5 3.7 1366 formate dehydrogen  
 1367 65.5 3.7 1367 two-component syst  
 1368 65.5 3.7 1368 hypothetical prote  
 1369 65.5 3.7 1369 alanine transamina  
 1370 65.5 3.7 1370 aminopeptidase BH2  
 1371 65.5 3.7 1371 pl polypeptide - m  
 1372 65.5 3.7 1372 hypothetical prote  
 1373 65.5 3.7 1373 hypothetical prote  
 1374 65.5 3.7 1374 hypothetical prote  
 1375 65.5 3.7 1375 hypothetical prote  
 1376 65.5 3.7 1376 TyA protein - Yeas  
 1377 65.5 3.7 1377 TyA protein - Yeas  
 1378 65.5 3.7 1378 hypothetical prote  
 1379 65.5 3.7 1379 conserved hypothet  
 1380 65.5 3.7 1380 conserved respirat  
 1381 65.5 3.7 1381 hypothetical cell  
 1382 65.5 3.7 1382 EcoA system protei  
 1383 65.5 3.7 1383 hypothetical prote  
 1384 65.5 3.7 1384 hypothetical prote  
 1385 65.5 3.7 1385 protein F47D12.9 [  
 1386 65.5 3.7 1386 inositol-3-phospha  
 1387 65.5 3.7 1387 high mobility grou  
 1388 65.5 3.7 1388 probable ubiquitin  
 1389 65.5 3.7 1389 probable ubiquitin  
 1390 65.5 3.7 1390 methy1-accepting c  
 1391 65.5 3.7 1391 dihydrofolate redu  
 1392 65.5 3.7 1392 hypothetical prote  
 1393 65.5 3.7 1393 hypothetical prote  
 1394 65.5 3.7 1394 putative autotransp  
 1395 65.5 3.7 1395 dnaK-type molecula  
 1396 65.5 3.7 1396 probable serine/th  
 1397 65.5 3.7 1397 TonB-dependent rec  
 1398 65.5 3.7 1398 exo-alpha-sialidas  
 1399 65.5 3.7 1399 probable portal pr  
 1400 65.5 3.7 1400 probable bi-functi  
 1401 65.5 3.7 1401 probable ABC trans  
 1402 65.5 3.7 1402 hypothetical prote  
 1403 65.5 3.7 1403 hypothetical prote  
 1404 65.5 3.7 1404 hypothetical prote  
 1405 65.5 3.7 1405 DNA helicase-prima  
 1406 65.5 3.7 1406 hypothetical prote  
 1407 65.5 3.7 1407 translation elonga  
 1408 65.5 3.7 1408 hypothetical prote  
 1409 65.5 3.7 1409 core protein VP3 -  
 1410 65.5 3.7 1410  
 1411 65.5 3.7 1411  
 1412 65.5 3.7 1412  
 1413 65.5 3.7 1413  
 1414 65.5 3.7 1414  
 1415 65.5 3.7 1415  
 1416 65.5 3.7 1416

1417 65.5 3.7 921 2 S49965 probable membrane  
1418 65.5 3.7 946 1 A47299 ror-related recept  
1419 65.5 3.7 948 2 C75265 hexagonally packe  
1420 65.5 3.7 953 2 E84732 probable ligand-ga  
1421 65.5 3.7 956 2 JS0685 glutamate receptor  
1422 65.5 3.7 1051 2 G84316 ribonucleoside red  
1423 65.5 3.7 1052 2 B49120 protein-tyrosine k  
1424 65.5 3.7 1054 2 D70425 conserved hypotet  
1425 65.5 3.7 1066 2 AB1228 transporter, (to B  
1426 65.5 3.7 1066 2 AD1581 transporter, (to B  
1427 65.5 3.7 1068 1 JQ1329 sucrose-phosphate  
1428 65.5 3.7 1084 2 B64088 hemoglobin-binding  
1429 65.5 3.7 1091 2 A58532 glial cell membran  
1430 65.5 3.7 1100 1 DDBYD1 RAD1 protein - yea  
1431 65.5 3.7 1125 2 H87644 TonB-dependent rec  
1432 65.5 3.7 1132 2 AD1809 phycobilisome core  
1433 65.5 3.7 1174 2 A40853 potassium channel  
1434 65.5 3.7 1259 2 S36126 neural cell adhesi  
1435 65.5 3.7 1270 2 T51227 related to verruco  
1436 65.5 3.7 1464 2 JC5144 murinoglobulin pre  
1437 65.5 3.7 1476 2 JC5143 alpha-macroglobuli  
1438 65.5 3.7 1487 2 AG2560 hypothetical prote  
1439 65.5 3.7 1657 2 T15938 hypothetical prote  
1440 65.5 3.7 1744 2 JH0720 tanabin - African  
1441 65.5 3.7 1755 2 S45736 TyB protein - yeas  
1442 65.5 3.7 1871 2 S27938 hypothetical prote  
1443 65.5 3.7 2062 2 G96602 probable receptor  
1444 65.5 3.7 2311 1 TVCHSR kinase-related pro  
1445 65.5 3.7 2386 2 T39911 rad3 checkpoint pr  
1446 65.5 3.7 3135 2 A48584 transmission block  
1447 65.5 3.7 3147 2 T21328 hypothetical prote  
1448 65.5 3.7 4302 2 A38971 polycystic kidney  
1449 65 3.7 61 2 F26420 T-cell receptor ga  
1450 65 3.7 115 1 KVM5K2 Ig kappa chain pre  
1451 65 3.7 128 1 KVM5T1 Ig kappa chain pre  
1452 65 3.7 140 2 I46638 rearranged T-cell  
1453 65 3.7 158 2 D83809 transcription elon  
1454 65 3.7 216 2 JEB0245 Ig lambda chain NI  
1455 65 3.7 219 2 T02114 hypothetical prote  
1456 65 3.7 231 1 A29459 orotate phosphorib  
1457 65 3.7 235 2 S25758 Ig lambda chain -  
1458 65 3.7 244 2 I62393 outer membrane pro  
1459 65 3.7 244 2 I62389 outer membrane pro  
1460 65 3.7 255 1 S48146 mucin 1 precursor,  
1461 65 3.7 273 2 T42928 immediate-early pr  
1462 65 3.7 308 2 C84072 UDP-glucose 4-epim  
1463 65 3.7 313 2 B69588 L-arabinose transp  
1464 65 3.7 322 2 PS0019 Ig gamma-2a chain  
1465 65 3.7 331 2 G91133 probable collagena  
1466 65 3.7 331 2 B85979 probable collagena  
1467 65 3.7 331 2 B65106 probable proteinas  
1468 65 3.7 345 2 A46052 vascular cell adhe  
1469 65 3.7 349 1 A28658 nitrilase (EC 3.5.  
1470 65 3.7 350 2 D84923 probable exonuclea  
1471 65 3.7 354 2 A81728 conserved hypotet  
1472 65 3.7 355 2 S21057 recf protein - Sal  
1473 65 3.7 358 2 G70601 hypothetical prote  
1474 65 3.7 363 2 B65057 hypothetical prote  
1475 65 3.7 373 1 VGBETC glycoprotein A - t  
1476 65 3.7 388 1 EHMS Ig epsilon chain C  
1477 65 3.7 392 2 S04205 protein-tyrosine k  
1478 65 3.7 394 2 B70411 fibrial assembly  
1479 65 3.7 397 2 T31803 hypothetical prote  
1480 65 3.7 404 2 F86517 hypothetical prote  
1481 65 3.7 404 2 G72106 hypothetical prote  
1482 65 3.7 412 2 E65146 hypothetical 47.4  
1483 65 3.7 414 2 S43340 glyceraldhyde-3-p  
1484 65 3.7 414 2 AB1500 N-carbamyl-L-amino  
1485 65 3.7 416 1 A42879 advanced glycosyla  
1486 65 3.7 425 2 D70436 DNA mismatch repai  
1487 65 3.7 432 1 RWCZT4 T-cell surface gly  
1488 65 3.7 443 1 E64667 multidrug-efflux t  
1489 65 3.7 443 2 T17970 hypothetical prote

1490 65 3.7 444 1 DYBOD2 dopamine receptor  
1491 65 3.7 444 2 PC4436 monoclonal antibod  
1492 65 3.7 449 2 A86643 serine proteinase  
1493 65 3.7 451 2 T33763 hypothetical prote  
1494 65 3.7 452 2 G95306 putrescine/ornithi  
1495 65 3.7 468 2 T49682 hypothetical prote  
1496 65 3.7 469 2 S50584 probable phosphogl  
1497 65 3.7 487 2 A12692 conserved hypotet  
1498 65 3.7 487 2 E97474 BH3939 hypotetica  
1499 65 3.7 493 2 T01206 cysteine proteinas  
1500 65 3.7 494 2 A35551 cytochrome P450 2G

## ALIGNMENTS

## RESULT 1

A46500

LY-9.2 antigen - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

C:Accession: A46500

R:Sandrin, M.S.; Gumley, T.P.; Henning, M.M.; Vaughan, H.A.; Gonez, L.J.; Trapani, J.A.

J. Immunol. 149, 1636-1641, 1992

A:Title: Isolation and characterization of cDNA clones for mouse Ly-9.

A:Reference number: A46500; MUID:92373005; PMID:1506686

A:Accession: A46500

A&gt;Status: preliminary

A:Molecule type: mRNA; protein

A:Residues: 1-629 &lt;SAN&gt;

A:Cross-references: GB:M84412; NID:G198931; PIDN:AAA39468.1; PID:G198932

A:Experimental source: C57BL/6

A&gt;Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIP:111654)

C:Keywords: transmembrane protein

Query: Match 19.4%; Score 343; DB 2; Length 629;  
Best Local Similarity 29.3%; Pred. No. 38-20; Indels 52; Gaps 14;  
Matches 105; Conservative 58; Mismatches 143

## QY

14 LMQL-TGSA- ---ASGPVKELVSGVGAFTPLKSK-VKQVDSIVMTFTNTPLVTIQTPEG 67

217 INQFCTGASRRKTAAG--KTVVGILGEPVTLPEFRATKTNVWVLTNS--VISQERR 272

## Db

68 GTIIVTQNR-----NRERVDPPDGGVSLKSLKKNDSIYVYGVSSLOQPSTQEVYL 122

273 GAATADSRKPKGSEERRVTSDDQSLKISQLKMDAGFYHAYVCSEASRDPVSRHFTL 332

## QY

123 HYVEHLSPKVTMGLOSKNKGTCVTNLTCCMEHGEEDVIYTWKALQQAANESHGSLPI 182

333 LVYKLEKPSVTKSPVHMNGICEVVLTCSDGGGNNVTYTWPLQNKAVMSGKSHLVN 392

## Db

183 SWRWGESDMTFTICVARNPVSRNFFSPILARKLCEGAADDPDSSMVLICLLVPLLSLFV 242

393 SWESGEHLNPNFTAHNPVS-NSSQPSGTCISG---PERNKRFWLLLVLLMLLI 447

## QY

243 LGLFWLFLKREQOEYIEEK-KRVDICRETPNICPHSG-----ENTE 283

448 GGYFI-LRKQKCSLATRYRQAEVPAEIPF-PPTGHGQFVSLRSQRYEKLMSAKTR 503

## QY

284 Y-----DTIPHTNFTLKEDPANTYVPEIPKMNPHSLTTPDTPRLPAYENVI 335

504 HQPTPTSDTSSSSATTEDEDEKTRHSTANGRNQL---YDLVTHQDTIAHALAYEQV 558

## RESULT 2

S58892

signaling lymphocytic activation molecule - human

C:Species: Homo sapiens (man)

C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C:Accession: S58892

R:Cocks, B.G.; Chang, C.C.; Carballido, J.M.; Yssel, H.; de Vries, J.E.; Aversa, G.

Nature 376, 260-263, 1995

A:Title: A novel receptor involved in T-cell activation.



[illegible]



```
RESULT 9
JH0395
Biliary glycoprotein h precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JH0395
R:Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A:Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr
A:Reference number: JH0394; MUID:91222218; PMID:2025273
A:Accession: JH0395
A:Molecule type: mRNA
A:Residues: 1-321 <KUR>
A:Cross-references: UNIPROT:PI3688; GB:M69176; NID:g179434; PID:AAA51825.1; PID:g179435
A:Experimental source: leukocyte
C:Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C:Keywords: glycoprotein; transmembrane protein
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-321/Product: biliary glycoprotein h #status predicted <MAT>
F:160-217/Domain: immunoglobulin homology <IMM1>
F:252-301/Domain: immunoglobulin homology <IMM2>

Query Match 7.1%; Score 125.5; DB 2; Length 321;
Best Local Similarity 25.1%; Pred. No. 0.01;
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

QY 68 GTIIVTQ-----NRRNRVDFPDGGYSLKSLKKNDSGIYVGYSSSL-QQPSTOE 119
DB 81 GYAIGTQQAATPGPANSGRGTI-YPNA--SLLQNTQNTDGTFTLVQIKSDLVNEATGQ 137
QY 120 YVLHVYHLSPKVTMGLQSNKNGTCVTNLTCMEHGEDVITYWKALGOAANESHNGSI 179
DB 138 F--HVYPPELPKPSISSNNSNPVEDKDAVFTC--EPETQDTTYLWMI-----NNQS 184
QY 180 LPISNRW-----GESDMTFICVAR-----NPVSRNFSPIARLKLCEG-----A 218
DB 185 LPVSPRLQLSNGNRITLLSVTRNDTGPYECIQNPVSNRSDPV-TLVNTYGPDPPTTIS 243
QY 219 ADD----PDSSMVLCLLL--VPLLISLFLVGLFLWFLKREQEYIEEKRVDCRETP 272
DB 244 PSDTYRPGANISLSCYAASNPAPQYSLWINGTF----QOSTQELFI-----P 287
QY 273 NI--CPHSGENTY--DTPIHTNRTILK 296
DB 288 NITVNSGSGYTCNANSVTGCNRTTVK 314

Query Match 7.1%; Score 125.5; DB 2; Length 321;
Best Local Similarity 25.1%; Pred. No. 0.01;
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

QY 68 GTIIVTQ-----NRRNRVDFPDGGYSLKSLKKNDSGIYVGYSSSL-QQPSTOE 119
DB 81 GYAIGTQQAATPGPANSGRGTI-YPNA--SLLQNTQNTDGTFTLVQIKSDLVNEATGQ 137
QY 120 YVLHVYHLSPKVTMGLQSNKNGTCVTNLTCMEHGEDVITYWKALGOAANESHNGSI 179
DB 138 F--HVYPPELPKPSISSNNSNPVEDKDAVFTC--EPETQDTTYLWMI-----NNQS 184
QY 180 LPISNRW-----GESDMTFICVAR-----NPVSRNFSPIARLKLCEG-----A 218
DB 185 LPVSPRLQLSNGNRITLLSVTRNDTGPYECIQNPVSNRSDPV-TLVNTYGPDPPTTIS 243
QY 219 ADD----PDSSMVLCLLL--VPLLISLFLVGLFLWFLKREQEYIEEKRVDCRETP 272
DB 244 PSDTYRPGANISLSCYAASNPAPQYSLWINGTF----QOSTQELFI-----P 287
QY 273 NI--CPHSGENTY--DTPIHTNRTILK 296
DB 288 NITVNSGSGYTCNANSVTGCNRTTVK 314

RESULT 10
JH0396
Biliary glycoprotein i precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JH0396
R:Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A:Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr
A:Reference number: JH0394; MUID:91222218; PMID:2025273
A:Accession: JH0396
A:Molecule type: mRNA
A:Residues: 1-351 <KUR>
A:Cross-references: UNIPROT:PI3688; GB:M72238; NID:g179436; PID:AAA58393.1; PID:g179437
A:Experimental source: leukocyte
C:Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C:Keywords: glycoprotein; transmembrane protein
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-351/Product: biliary glycoprotein i #status predicted <MAT>
F:160-217/Domain: immunoglobulin homology <IMM1>
```

```
F:252-301/Domain: immunoglobulin homology <IMM2>

Query Match 7.1%; Score 125.5; DB 2; Length 351;
Best Local Similarity 25.1%; Pred. No. 0.012;
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

QY 68 GTIIVTQ-----NRRNRVDFPDGGYSLKSLKKNDSGIYVGYSSSL-QQPSTOE 119
DB 81 GYAIGTQQAATPGPANSGRGTI-YPNA--SLLQNTQNTDGTFTLVQIKSDLVNEATGQ 137
QY 120 YVLHVYHLSPKVTMGLQSNKNGTCVTNLTCMEHGEDVITYWKALGOAANESHNGSI 179
DB 138 F--HVYPPELPKPSISSNNSNPVEDKDAVFTC--EPETQDTTYLWMI-----NNQS 184
QY 180 LPISNRW-----GESDMTFICVAR-----NPVSRNFSPIARLKLCEG-----A 218
DB 185 LPVSPRLQLSNGNRITLLSVTRNDTGPYECIQNPVSNRSDPV-TLVNTYGPDPPTTIS 243
QY 219 ADD----PDSSMVLCLLL--VPLLISLFLVGLFLWFLKREQEYIEEKRVDCRETP 272
DB 244 PSDTYRPGANISLSCYAASNPAPQYSLWINGTF----QOSTQELFI-----P 287
QY 273 NI--CPHSGENTY--DTPIHTNRTILK 296
DB 288 NITVNSGSGYTCNANSVTGCNRTTVK 314

RESULT 11
JH0394
Biliary glycoprotein g precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JH0394
R:Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A:Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr
A:Reference number: JH0394; MUID:91222218; PMID:2025273
A:Accession: JH0394
A:Molecule type: mRNA
A:Residues: 1-417 <KUR>
A:Cross-references: UNIPROT:PI3688; GB:M72238; NID:g179436; PID:AAA58394.1; PID:g17943
A:Experimental source: leukocyte
C:Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C:Keywords: glycoprotein; transmembrane protein
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-383/Product: biliary glycoprotein g #status predicted <MAT>
F:160-217/Domain: immunoglobulin homology <IMM1>
F:252-301/Domain: immunoglobulin homology <IMM2>
F:341-398/Domain: immunoglobulin homology <IMM3>

Query Match 7.1%; Score 125.5; DB 2; Length 417;
Best Local Similarity 25.1%; Pred. No. 0.014;
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

QY 68 GTIIVTQ-----NRRNRVDFPDGGYSLKSLKKNDSGIYVGYSSSL-QQPSTOE 119
DB 81 GYAIGTQQAATPGPANSGRGTI-YPNA--SLLQNTQNTDGTFTLVQIKSDLVNEATGQ 137
QY 120 YVLHVYHLSPKVTMGLQSNKNGTCVTNLTCMEHGEDVITYWKALGOAANESHNGSI 179
DB 138 F--HVYPPELPKPSISSNNSNPVEDKDAVFTC--EPETQDTTYLWMI-----NNQS 184
QY 180 LPISNRW-----GESDMTFICVAR-----NPVSRNFSPIARLKLCEG-----A 218
DB 185 LPVSPRLQLSNGNRITLLSVTRNDTGPYECIQNPVSNRSDPV-TLVNTYGPDPPTTIS 243
QY 219 ADD----PDSSMVLCLLL--VPLLISLFLVGLFLWFLKREQEYIEEKRVDCRETP 272
DB 244 PSDTYRPGANISLSCYAASNPAPQYSLWINGTF----QOSTQELFI-----P 287
QY 273 NI--CPHSGENTY--DTPIHTNRTILK 296
```







F;35-319,'D',417-526/Product: biliary glycoprotein 1, splice form b #status predicted <M>  
F;35-141,'H',417-526/Product: biliary glycoprotein 1, splice form x #status predicted <M>  
F;160-217/Domain: immunoglobulin homology <IMM1>  
F;452-301/Domain: immunoglobulin homology <IMM2>  
F;341-398/Domain: immunoglobulin homology <IMM3>  
F;425-454/Domain: transmembrane #status predicted <TM>  
F;453-526/Domain: intracellular #status predicted <INT>  
F;104,111,115,152,182,197,208,224,232,254,274,288,292,302,309,345,351,363,378,405,475/Bi

Query Match 7.1%; Score 125.5; DB 1; Length 526;  
Best Local Similarity 25.1%; Pred. No. 0.019;  
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

QY 68 GTIIVTQ-----NNRRERVDPPDGGYSLSKLKNDSDGIYVGYSSSI-QQSTQIE 119  
Db GVAIGTQQATPGPANGRETI-YPNA--SLIIQNTQNDTGFTLQVIKSDLVNERATQ 137

QY 120 YVLHYVYHLSKPKVTMGLOSNGKGTCTNLTCMEHGEEDVIYTWKALQQAENSHGSI 179  
Db F--HVYPPEPKPSISSNNSNPVEDKDAVFTC--EPETQDTYLVWI-----NNQS 184

QY 180 LPISWRW-----GESDMTFICVAR-----NPVSRNFSPIIARKLCGE-----A 218  
Db LPVSPRLQLSNGNRITLLSVTRNDTPGYECIEQNPVSANRSPV-TLVNTYGPDPPTIS 243

QY 219 ADD----PDSMVLLCLLL--VPLLSLVFLGLFLFKRQEEVIEKKRVDCRETP 272  
Db PSDTYRPGANLSLSYASNPAPQSWLNGTF----QOSTQELFI-----P 287

QY 273 NT-CPHSNTYNT--DTIHTNRTILK 296  
Db NTVNNSGGYTCNANSVTCNRTTVK 314

RESULT 14  
A27681  
non-specific cross-reacting antigen precursor - human  
N/Alternate names: NCA; TEX/NCA  
C/Species: Homo sapiens (man)  
C/Date: 31-Mar-1989 #sequence revision 16-Sep-1992 #text change 09-Jul-2004  
C/Accession: A26902; A29875; A27681; B31037; A29918; A27709; A36271; C26414; E44476; F44  
R/Oikawa, S.; Kosaki, G.; Nakazato, H.  
Biochem. Biophys. Res. Commun. 146, 464-469, 1987  
A/Title: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) gene  
A/Reference number: A26902; MUID:87298464; PMID:3619891  
A/Accession: A26902  
A/Molecule type: DNA  
A/Residues: 1-141 <OIK>  
A/Cross-references: UNIPROT:Q13774; GB:M17082; NID:G180230; PIDN:AAAS1971.1; PID:G553222  
R/Thompson, J.A.; Pande, H.; Faxton, R.J.; Shively, L.; Padma, A.; Simmer, R.L.; Todd, C  
Proc. Natl. Acad. Sci. U.S.A. 84, 2965-2969, 1987  
A/Title: Molecular cloning of a gene belonging to the carcinoembryonic antigen gene fami  
A/Reference number: A29875; MUID:87204248; PMID:3033672  
A/Accession: A29875  
A/Molecule type: DNA  
A/Residues: 23-141 <THO>  
A/Cross-references: GB:M16337  
A/Note: the authors translated the codon ACT for residue 64 as Tyr  
R/Tawaragi, Y.; Oikawa, S.; Matsuka, Y.; Kosaki, G.; Nakazato, H.  
Biochem. Biophys. Res. Commun. 150, 89-96, 1988  
A/Title: Primary structure of non-specific crossreacting antigen (NCA), a member of carci  
A/Reference number: A27681; MUID:88106638; PMID:3337731  
A/Accession: A27681  
A/Molecule type: mRNA  
A/Residues: 1-238,'V',240-344 <TAW>  
A/Cross-references: GB:M18728; NID:G189084; PIDN:AAAS9907.1; PID:G189085  
R/Barnett, T.; Goebel, S.G.; Nothdurft, W.A.; Elting, J.J.  
Genomics 3, 59-66, 1988  
A/Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and C  
A/Reference number: A31037; MUID:89122014; PMID:3220478  
A/Accession: B31037  
A/Molecule type: mRNA  
A/Residues: 1-137,'L',139-344 <BAR>

A/Cross-references: GB:M29541; NID:G189103; PIDN:AAAS9915.1; PID:G189104  
A/Note: the authors translated the codon TTG for residue 138 as Phe  
R/Neumaier, M.; Zimmermann, W.; Shively, L.; Hinoda, Y.; Riggs, A.D.; Shively, J.E.  
J. Biol. Chem. 263, 3202-3207, 1988  
A/Title: Characterization of a cDNA clone for the non-specific cross-reacting antigen (N  
A/Reference number: A29918; MUID:88139389; PMID:2830274  
A/Accession: A29918  
A/Molecule type: mRNA  
A/Residues: 1-344 <NEU>  
A/Cross-references: GB:M18216; GB:J03550; NID:G178690; PIDN:AAAS1739.1; PID:G178691  
R/Gruber, F.; Kolbinger, F.; Schwarz, K.; Schwaiblmair, H.; von Kleist, S.  
Biochem. Biophys. Res. Commun. 153, 1105-1115, 1988  
A/Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and in  
A/Reference number: A27709; MUID:88268882; PMID:3390172  
A/Accession: A27709  
A/Molecule type: protein  
A/Residues: 35-95;99-120;123-138;149-151,'X',153-162;166,'X',168-172,'X',174-193;231-23  
R/Hefla, S.A.; Paxton, R.J.; Shively, J.E.  
J. Biol. Chem. 265, 8618-8626, 1990  
A/Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspec  
A/Reference number: A36271; MUID:90256782; PMID:2341397  
A/Accession: A36271  
A/Molecule type: protein  
A/Residues: 35-42;44-53;55-80;83-134;139-160;166-172;174-180;191-194;204-224;233-308;31  
R/Paxton, R.J.; Mooser, G.; Pande, H.; Lee, T.D.; Shively, J.E.  
Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987  
A/Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation  
A/Reference number: A26414; MUID:87147209; PMID:3469650  
A/Accession: C26414  
A/Molecule type: protein  
A/Residues: 35-69 <PAX>  
R/Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Brener, K.; Hammarstrom, S.  
Genomics 14, 384-390, 1992  
A/Title: Identification of three new genes and estimation of the size of the carcinoemb  
A/Reference number: A44476; MUID:93052339; PMID:1427854  
A/Accession: E44476  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 35-141 <KHA>  
A/Accession: F44476  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 35-137,'L',139-141 <KH2>  
C/Comment: This protein appears to be processed at the carboxyl terminus and anchored t  
C/Genetics:  
A/Gene: GDB:NCA  
A/Cross-references: GDB:120231; OMIM:163980  
A/Map position: 19q13.2-19q13.2  
A/Introns: 22/1  
A/Note: the list of introns may be incomplete  
C/Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi  
C/Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphat  
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>  
F;1-34/Domain: signal sequence #status predicted <SIG>  
F;35-320/Product: non-specific cross-reacting antigen #status experimental <MAT>  
F;160-217/Domain: immunoglobulin homology <IMM1>  
F;252-301/Domain: immunoglobulin homology <IMM2>  
F;321-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F;104,111,115,152,173,197,224,256,274,288,292/Binding site: carbohydrate (Asn) (covalen  
F;309/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;320/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature for

Query Match 7.0%; Score 124.5; DB 2; Length 344;  
Best Local Similarity 22.4%; Pred. No. 0.014;  
Matches 75; Conservative 35; Mismatches 118; Indels 107; Gaps 16;

QY 53 WTFNTPLVTIQ-----PEGGTII-----VTQNR-----NRERVD----- 82  
Db WNPPTTAKLTISTEPFNAEGKVELLAHNLFPQRIIGYSWYKGERVDGNSLIVGYVIGTQ 87

QY 83 ---FPDGGY-----SLKLSKLKNDSDGIYVGYSSSI-QQPSTQYVLHVYHLS 129  
Db QATPGPAYSGRETIYPNASLLIQNTQNDTGFTLQVIKSDLVNEBATGQF--HVYPPEL 145



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 14, 2005, 13:19:12 ; Search time 63 seconds  
(without alignments)  
2722.961 Million cell updates/sec

Title: US-10-063-551-46

Perfect score: 1772

Sequence: 1 MAGSPCTLLIYLWLQGTG.....PHSLLTMPDTPRLFAVENVI 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Uniprot 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1772	100.0	335	2 Q9NC25	Q9nc25 homo sapien
2	1769	99.8	335	2 Q9NY08	Q9ny08 homo sapien
3	1392.5	78.6	328	2 Q9NY23	Q9ny23 homo sapien
4	1349	76.1	296	2 Q8NCY8	Q8ncy8 homo sapien
5	1160.5	65.5	228	2 Q8ND32	Q8nd32 homo sapien
6	817	46.1	333	2 Q8BHK6	Q8bhk6 m mus muscu
7	778.5	43.9	335	2 Q8CJ64	Q8cj64 mus musculus
8	773.5	43.7	335	2 Q8BTL2	Q8btl2 mus musculus
9	769.5	43.4	335	2 Q8CJ65	Q8cj65 mus musculus
10	651	36.7	300	2 Q8CJ63	Q8cj63 mus musculus
11	637.5	36.0	294	2 Q91XA0	Q91xa0 mus musculus
12	362.5	20.5	328	2 Q15430	Q15430 homo sapien
13	362.5	20.5	329	2 Q9Z178	Q9z178 mus musculus
14	359	20.3	339	2 Q8WW18	Q8ww18 homo sapien
15	358.5	20.2	645	2 Q6NZB6	Q6nzb6 mus musculus
16	358	20.2	345	2 Q9UIB8	Q9uib8 homo sapien
17	354.5	20.0	328	2 Q6FHA8	Q6fha8 homo sapien
18	354.5	20.0	649	2 Q7TMP7	Q7tmp7 mus musculus
19	354.5	20.0	654	1 LY9_MOUSE	Q01965 mus musculus
20	353.5	19.9	544	2 Q8C2D4	Q8c2d4 mus musculus
21	330.5	18.7	289	2 Q96A28	Q96a28 homo sapien
22	329	18.6	538	2 Q8C9E4	Q8c9e4 mus musculus
23	318	17.9	655	1 LY9_HUMAN	Q9hbq7 homo sapien
24	311.5	17.6	285	2 Q8BTK0	Q8btk0 mus musculus
25	311	17.6	332	1 SLF6_HUMAN	Q96du3 homo sapien
26	308.5	17.4	285	2 Q8VE93	Q8ve93 mus musculus
27	308	17.4	280	2 Q95660	Q95660 homo sapien
28	307.5	17.4	285	2 Q9D780	Q9d780 mus musculus
29	304	17.2	272	2 Q9UIB7	Q9uib7 homo sapien
30	290.5	16.4	241	2 Q9UIB6	Q9uib6 homo sapien
31	281	15.9	197	2 Q9UI17	Q9uit7 homo sapien

32	225.5	12.7	351	1 SLF6_MOUSE	Q9et39 mus musculus
33	204.5	11.5	338	2 Q95MM6	Q95mm6 bos taurus
34	187.5	10.6	336	2 Q9GJT3	Q9gjt3 saguinus oe
35	186	10.5	343	1 SLAM_MOUSE	Q9qum4 mus musculus
36	183.5	10.4	335	2 Q96QR3	Q96qr3 homo sapien
37	183	10.3	266	2 Q9CUC8	Q9cuc8 mus musculus
38	182.5	10.3	335	1 SLAM_HUMAN	Q13291 homo sapien
39	179	10.1	278	2 Q9D3G2	Q9d3g2 mus musculus
40	178	10.0	278	2 Q8B3T7	Q8b3t7 mus musculus
41	168.5	9.5	342	2 Q9SL99	Q9sl99 canis famil
42	167.5	9.5	342	2 Q95MM9	Q95mm9 canis famil
43	163.5	9.2	370	1 C244_HUMAN	Q9bzw8 homo sapien
44	158.5	8.9	326	2 Q8CAU4	Q8cau4 mus musculus
45	152	8.6	288	2 Q9NQ26	Q9nq26 homo sapien
46	150.5	8.5	285	2 Q9P0V8	Q9p0v8 homo sapien
47	145.5	8.2	416	2 Q8N7I3	Q8n7i3 homo sapien
48	145.5	8.2	416	2 Q67IP8	Q67ip8 homo sapien
49	145	8.2	211	2 Q6ZRI7	Q6zri7 homo sapien
50	144	8.1	344	1 CD2_MOUSE	Q08920 mus musculus
51	144	8.1	344	2 Q9R201	Q9r201 mus musculus
52	142	8.0	207	2 Q9HBE9	Q9hbe9 homo sapien
53	142	8.0	367	2 Q6ZW14	Q6zwl4 homo sapien
54	138.5	7.8	340	2 Q764N3	Q764n3 sus scrofa
55	138.5	7.8	413	2 Q64OR3	Q64or3 mus musculus
56	137.5	7.8	345	2 Q6S2G3	Q6szg3 pan troglod
57	135.5	7.6	289	2 Q6QX36	Q6qx36 mus musculus
58	134.5	7.6	198	2 Q6UWGI	Q6uugi homo sapien
59	134	7.6	240	1 CD48_RAT	P10252 rattus norv
60	133.5	7.5	351	1 CD2_HUMAN	P06729 homo sapien
61	133.5	7.5	394	2 Q9EQK9	Q9eqk9 rattus norv
62	132.5	7.5	372	2 Q9OY50	Q9oy50 brachydanio
63	130	7.3	344	1 CD2_RAT	P08921 rattus norv
64	128.5	7.3	253	2 Q28753	Q28753 ovib sp. lf
65	128	7.2	193	2 Q6P2J4	Q6p2j4 homo sapien
66	126.5	7.1	240	1 CD48_MOUSE	P18181 mus musculus
67	126.5	7.1	240	2 Q6P905	Q6p905 mus musculus
68	126.5	7.1	290	2 Q7M5D4	Q7m5d4 avian adeno
69	125.5	7.1	464	2 Q16170	Q16170 homo sapien
70	125.5	7.1	468	2 Q96CA7	Q96ca7 homo sapien
71	125.5	7.1	526	1 CEAL_HUMAN	P13688 homo sapien
72	125	7.1	344	2 Q6S2G2	Q6szg2 papio anubi
73	125	7.1	373	2 Q7KVP5	Q7kvp5 homo sapien
74	124.5	7.0	344	1 CEAG_HUMAN	P40199 homo sapien
75	124.5	7.0	344	2 Q13774	Q13774 homo sapien
76	124.5	7.0	461	2 Q13854	Q13854 homo sapien
77	124	7.0	345	2 Q6S258	Q6sz58 macaca asca
78	123.5	6.9	227	2 Q28754	Q28754 ovib sp. lf
79	123	6.9	140	2 Q8BFW0	Q8bfw0 m mus muscu
80	123	6.9	211	1 C244_RAT	Q9jlm2 rattus norv
81	122.5	6.9	298	2 Q804R4	Q804r4 brachydanio
82	122.5	6.9	458	2 Q61351	Q61351 mus musculus
83	122.5	6.9	521	2 Q61352	Q61352 mus musculus
84	122	6.9	326	2 Q9N166	Q9n166 papio hamad
85	122	6.9	334	2 Q6SZ56	Q6sz56 macaca neme
86	122	6.9	341	2 Q6SZ57	Q6sz57 macaca arct
87	122	6.9	344	2 Q9UKV4	Q9ukv4 homo sapien
88	121.5	6.9	536	2 Q8BVE2	Q8bv2 mus musculus
89	121.5	6.9	351	2 Q6SZ61	Q6sz61 macaca fasc
90	121	6.8	351	2 Q6SZ61	Q6sz61 macaca fasc
91	119.5	6.7	332	2 Q91B08	Q91b08 phaeooides
92	119.5	6.7	365	1 CXAR_HUMAN	P78310 homo sapien
93	118.5	6.7	520	2 Q925F2	Q925f2 mus musculus
94	118.5	6.6	319	1 A33_HUMAN	Q99795 homo sapien
95	116.5	6.6	350	2 Q6SZ60	Q6sz60 cercocobus
96	115	6.5	351	2 Q6SZ60	Q6sz60 macaca mula
97	115	6.5	357	2 Q90ZL5	Q90z15 anas platyr
98	114.5	6.5	430	2 Q8N4F1	Q8n4f1 homo sapien
99	114.5	6.5	702	1 CEAS_HUMAN	P06731 homo sapien
100	114.5	6.5	454	2 Q8N4D0	Q8n4d0 homo sapien
101	113.5	6.4	454	2 Q91W54	Q91w54 mus musculus
102	113.5	6.4	521	1 CEAL_MOUSE	P31809 mus musculus
103	113.5	6.4	521	2 Q925P3	Q925p3 mus musculus
104	113	6.4	373	2 Q9H6B4	Q9h6b4 homo sapien

105	113	6.4	621	2	Q811T7	Q811T7 mus musculus	178	97	5.5	484	2	Q26475	Q26475 schistocerc
106	111	6.3	372	2	Q8K1G0	Q8K1G0 rattus norv	179	97	5.5	773	1	PIGR_RABIT	P01832 oryctolagus
107	110.5	6.2	391	2	Q7QJG1	Q7QJG1 anopheles g	180	96.5	5.4	368	2	Q6RWT3	Q6RWT3 bos taurus
108	110.5	6.2	463	1	CD4_CANFA	P33705 canis famli	181	96.5	5.4	375	2	Q6RWT4	Q6RWT4 bos taurus
109	110	6.2	539	2	Q8HXQ6	Q8HXQ6 sus scrofa	182	96.5	5.4	402	2	Q89501	Q89501 african swi
110	109.5	6.2	432	2	Q6LBN1	Q6LBN1 canis famli	183	96.5	5.4	432	2	Q6RWT5	Q6RWT5 bos taurus
111	109	6.2	316	2	Q8VE98	Q8VE98 mus musculus	184	96.5	5.4	439	2	Q6RWT6	Q6RWT6 bos taurus
112	108.5	6.1	365	2	Q8WMV3	Q8WMV3 bos taurus	185	96.5	5.4	493	2	Q6P5Y4	Q6P5Y4 homo sapien
113	108	6.1	316	2	Q9CVA4	Q9CVA4 mus musculus	186	96.5	5.4	533	2	Q8NCB6	Q8NCB6 homo sapien
114	108	6.1	304	2	Q7TPB4	Q7TPB4 rattus norv	187	96.5	5.4	534	2	Q8NCB8	Q8NCB8 homo sapien
115	107	6.0	399	2	Q9SESE5	Q9SESE5 mus musculus	188	96.5	5.4	1896	2	Q9IAJ1	Q9IAJ1 xenopus lae
116	106.5	6.0	752	2	Q9XYS4	Q9XYS4 hydra atten	189	96	5.4	339	2	Q9IAZ7	Q9IAZ7 spheeroides
117	106.5	6.0	4138	2	Q811Y3	Q811Y3 plasmodium	190	96	5.4	341	2	Q61354	Q61354 mus musculus
118	106	6.0	897	2	Q867Y2	Q867Y2 arabidopsis	191	96	5.4	359	1	LACH_DROME	Q24372 drosophila
119	105.5	6.0	329	1	CD66_HUMAN	P42081 homo sapien	192	96	5.4	359	2	Q9V6C2	Q9V6C2 drosophila
120	105.5	6.0	335	2	Q9PWK4	Q9PWK4 gallus gall	193	96	5.4	526	1	BUTY_HUMAN	Q13410 homo sapien
121	105.5	6.0	398	2	Q9JIE1	Q9JIE1 mus musculus	194	96	5.4	526	2	Q9H458	Q9H458 homo sapien
122	105	5.9	397	1	C244_MOUSE	Q07763 mus musculus	195	96	5.4	1087	1	PGDS_XENLA	P28619 xenopus lae
123	104.5	5.9	319	2	Q9TU79	Q9TU79 sus scrofa	196	96	5.4	1451	1	MYM1_HUMAN	P52179 homo sapien
124	104.5	5.9	1271	2	Q8A321	Q8A321 bacteroides	197	96	5.4	1685	2	Q6H969	Q6H969 homo sapien
125	104	5.9	455	2	Q920L8	Q92018 mus musculus	198	96	5.4	1685	2	Q6ZUU0	Q6ZUU0 homo sapien
126	104	5.9	535	2	Q9EQT7	Q9EQT7 mus musculus	199	95.5	5.4	248	2	Q9D0T4	Q9D0T4 mus musculus
127	104	5.9	1220	2	Q94191	Q94191 paracoccidi	200	95.5	5.4	304	2	Q6JHT7	Q6JHT7 african swi
128	103.5	5.8	319	2	Q9TU80	Q9TU80 canis famli	201	95.5	5.4	340	2	Q61349	Q61349 mus musculus
129	103.5	5.8	323	2	Q9BDB8	Q9BDB8 cercocobus	202	95.5	5.4	365	1	CXAR_MOUSE	P97792 mus musculus
130	103.5	5.8	373	2	Q8R373	Q8R373 mus musculus	203	95.5	5.4	365	2	Q9DBJ8	Q9DBJ8 rattus norv
131	103.5	5.8	406	2	Q8N7T8	Q8N7T8 homo sapien	204	95.5	5.4	448	2	Q9JHL7	Q9JHL7 rattus norv
132	103	5.8	1062	2	Q8AXC7	Q8AXC7 fugu rubrip	205	95.5	5.4	458	2	Q63093	Q63093 rattus norv
133	103	5.8	1078	2	Q8AXC8	Q8AXC8 fugu rubrip	206	95.5	5.4	459	2	Q9JHL6	Q9JHL6 rattus norv
134	103	5.8	1479	2	Q7KQT5	Q7KQT5 drosophila	207	95.5	5.4	463	2	Q66J72	Q66J72 xenopus lae
135	102.5	5.8	304	2	Q8JSP1	Q8JSP1 african swi	208	95.5	5.4	482	2	Q7Q815	Q7Q815 anopheles g
136	102.5	5.8	323	2	Q9BDM4	Q9BDM4 macaca mula	209	95.5	5.4	628	2	Q7S409	Q7S409 neurospora
137	102.5	5.8	335	2	Q9YGH1	Q9YGH1 gallus gall	210	95.5	5.4	700	1	PTPE_HUMAN	P23469 homo sapien
138	102.5	5.8	373	2	Q920S5	Q920S5 mus musculus	211	95.5	5.4	771	1	PIGR_MOUSE	Q70570 mus musculus
139	102.5	5.8	519	1	ECTO_RAT	P16573 rattus norv	212	95.5	5.4	822	1	CAN3_SHEEP	Q9T88 ovis aries
140	102	5.7	1482	2	Q9V4Y0	Q9V4Y0 drosophila	213	95.5	5.4	1684	2	Q7RIA5	Q7RIA5 plasmodium
141	101.5	5.7	761	2	Q22271	Q22271 arabidopsis	214	95	5.4	316	2	Q6UXI2	Q6UXI2 homo sapien
142	101	5.7	349	1	CEA8_HUMAN	P31997 homo sapien	215	95	5.4	814	2	Q8IVU1	Q8IVU1 homo sapien
143	101	5.7	349	1	LACH_SCHAM	Q26474 schistocerc	216	94.5	5.3	280	2	Q8UWK3	Q8UWK3 ictalurus p
144	101	5.7	365	2	Q6VAN5	Q6VAN5 bos taurus	217	94.5	5.3	286	2	O46535	O46535 bos taurus
145	101	5.7	372	2	Q6VAN6	Q6VAN6 bos taurus	218	94.5	5.3	379	2	O8BLX5	O8BLX5 mus musculus
146	101	5.7	429	2	Q6VAN7	Q6VAN7 bos taurus	219	94.5	5.3	397	2	Q8BFX8	Q8BFX8 m mus muscu
147	101	5.7	432	2	Q6DDE7	Q6DDE7 xenopus lae	220	94.5	5.3	588	2	Q6MG92	Q6MG92 rattus norv
148	101	5.7	436	2	Q6VAN8	Q6VAN8 bos taurus	221	94	5.3	233	1	GP42_RAT	P23505 rattus norv
149	101	5.7	588	1	C166_CHICK	P42292 gallus gall	222	94	5.3	336	2	Q8WNV8	Q8WNV8 felis silve
150	101	5.7	1637	2	Q6LOY1	Q6LOY1 picrophilus	223	94	5.3	344	2	Q8R067	Q8R067 rattus norv
151	100.5	5.7	259	2	Q9CFA4	Q9CFA4 lactococcus	224	94	5.3	419	2	Q96QL5	Q96QL5 homo sapien
152	100.5	5.7	280	2	Q8UWL2	Q8UWL2 ictalurus p	225	94	5.3	828	1	Q8C8T7	Q8C8T7 mus musculus
153	100.5	5.7	323	2	Q9BDM2	Q9BDM2 cercopithec	226	94	5.3	1088	1	NCA1_XENLA	P16170 xenopus lae
154	100.5	5.7	555	1	C166_CARAU	Q90304 carassius a	227	93.5	5.3	358	2	Q9R066	Q9R066 rattus norv
155	100	5.6	324	2	Q6JHT1	Q6JHT1 african swi	228	93	5.2	270	2	Q6XJV4	Q6XJV4 mus musculus
156	99.5	5.6	323	2	Q9BDM9	Q9BDM9 macaca neme	229	93	5.2	316	2	Q9BXR1	Q9BXR1 homo sapien
157	99.5	5.6	335	2	Q9YGV5	Q9YGV5 gallus gall	230	93	5.2	339	2	Q7KRL5	Q7KRL5 drosophila
158	99.5	5.6	658	2	Q75JX6	Q75JX6 dictyosteli	231	93	5.2	342	2	Q9IB00	Q9IB00 spheeroides
159	99	5.6	417	1	PVR_CERAE	P32506 cercopithec	232	93	5.2	419	1	PSG4_HUMAN	Q00888 homo sapien
160	98.5	5.6	229	2	Q8BNV8	Q8BNV8 mus musculus	233	93	5.2	419	1	PSG7_HUMAN	Q13046 homo sapien
161	98.5	5.6	348	2	Q9GST1	Q9GST1 homo sapien	234	93	5.2	535	1	PVRG_SPICI	P52200 spiroplasma
162	98.5	5.6	404	2	Q9GZZ9	Q9GZZ9 homo sapien	235	93	5.2	752	2	Q9DGN6	Q9DGN6 gallus gall
163	98.5	5.6	526	1	BUTY_BOVIN	P18892 bos taurus	236	93	5.2	793	2	O70246	O70246 mus musculus
164	98.5	5.6	733	2	Q8SQ83	Q8SQ83 trichosurus	237	93	5.2	813	2	Q8BQC3	Q8BQC3 mus musculus
165	98.5	5.6	1227	2	Q21038	Q21038 caenorhabdi	238	93	5.2	949	2	Q6FKB0	Q6FKB0 candida gla
166	98.5	5.6	16215	2	Q9NFS3	Q9NFS3 drosophila	239	93	5.2	1788	2	Q9IAJ0	Q9IAJ0 xenopus lae
167	98	5.5	347	1	CD2_HORSE	P37998 equus cabal	240	92.5	5.2	160	2	Q8C239	Q8C239 mus musculus
168	98	5.5	484	2	Q6BE00	Q6BE00 xenopus lae	241	92.5	5.2	299	1	JAM1_HUMAN	Q9Y624 homo sapien
169	98	5.5	503	1	SHS1_HUMAN	P78124 h protein-t	242	92.5	5.2	330	1	CD86_RABIT	P42071 oryctolagus
170	98	5.5	1382	1	MET_RAT	P97523 rattus norv	243	92.5	5.2	344	2	Q6P660	Q6P660 homo sapien
171	97.5	5.5	562	2	Q6VNR7	Q6VNR7 brachydanio	244	92.5	5.2	344	2	Q8O1W5	Q8O1W5 brachydanio
172	97.5	5.5	591	2	Q6NP04	Q6NP04 drosophila	245	92.5	5.2	485	2	Q6UXG8	Q6UXG8 homo sapien
173	97.5	5.5	272	2	Q9VAV4	Q9VAV4 drosophila	246	92.5	5.2	535	2	O7ZZ85	Q7ZZ85 brachydanio
174	97.5	5.5	2776	2	Q869A0	Q869A0 drosophila	247	92.5	5.2	544	1	C166_BRARE	Q90460 brachydanio
175	97.5	5.5	2894	2	Q7KRX2	Q7KRX2 drosophila	248	92.5	5.2	564	2	Q61QX4	Q61QX4 brachydanio
176	97.5	5.5	2898	2	Q868Z9	Q868Z9 drosophila	249	92.5	5.2	760	2	Q8EBB5	Q8EBB5 shewanella
177	97	5.5	352	2	Q91W66	Q91W66 mus musculus	250	92.5	5.2	761	2	Q9C9S3	Q9C9S3 arabidopsis

251	92.5	5.2	777	2	Q7RAQ7	Q7rac7 plasmodium	324	89	5.0	240	2	Q9BRW0	Q9brw0 homo sapien
252	92.5	5.2	782	2	Q8JVB8	Q8jvb8 porcine lym	325	89	5.0	262	2	Q8OT70	Q8ot70 mus musculus
253	92.5	5.2	783	2	Q8B3U9	Q8b3u9 porcine lym	326	89	5.0	309	1	CD86_MOUSE	P42082 mus musculus
254	92	5.2	237	2	Q63476	Q63476 rattus norv	327	89	5.0	314	2	Q61238	Q61238 mus musculus
255	92	5.2	419	2	Q68CR6	Q68cr6 homo sapien	328	89	5.0	315	2	Q96DM5	Q96dm5 homo sapien
256	92	5.2	426	1	PSG8_HUMAN	Q9uq74 homo sapien	329	89	5.0	322	2	Q9PTR8	Q9ptr8 spherooides
257	92	5.2	609	2	Q9YKD7	Q9ykd7 rinderpest	330	89	5.0	323	2	Q8MKZ7	Q8mkz7 drosophila
258	92	5.2	700	1	KIR2_MOUSE	Q7tau7 mus musculus	331	89	5.0	325	2	Q95791	Q95791 homo sapien
259	92	5.2	743	2	Q6PIM7	Q6pim7 homo sapien	332	89	5.0	328	2	Q92109	Q92109 mus musculus
260	92	5.2	789	2	Q71512	Q71512 bacillus th	333	89	5.0	356	2	Q64381	Q64381 mus musculus
261	92	5.2	822	2	Q92QX3	Q92qx3 arabisopsis	334	89	5.0	434	2	Q6DN72	Q6dn72 homo sapien
262	92	5.2	1020	1	FRM4_MOUSE	Q8bie6 mus musculus	335	89	5.0	506	2	Q6MG91	Q6mg91 rattus norv
263	92	5.2	1025	2	Q7XTP6	Q7xtp6 cryza sativ	336	89	5.0	821	1	CAN3_HUMAN	P20807 homo sapien
264	92	5.2	1031	2	Q6PDJ4	Q6pdj4 mus musculus	337	89	5.0	5175	2	O810L3	O810l3 caenorhabdi
265	92	5.2	1087	2	Q7ZV71	Q7zv71 xenopus lae	338	89	5.0	5198	2	O76518	O76518 caenorhabdi
266	92	5.2	2828	2	Q9NR99	Q9nr99 homo sapien	339	88.5	5.0	271	1	OX2V_HHV8	P88963 human herpe
267	91.5	5.2	160	2	Q8C254	Q8c254 mus musculus	340	88.5	5.0	271	1	OX2V_HHV8	O40948 human herpe
268	91.5	5.2	226	2	O8NH11	O8nh11 homo sapien	341	88.5	5.0	315	2	Q9DGL5	Q9dgl5 gallus gall
269	91.5	5.2	230	2	O8UW30	O8uw30 brachydanio	342	88.5	5.0	325	2	O8UWL3	O8uwl3 ictalurus p
270	91.5	5.2	230	2	O90286	O90286 brachydanio	343	88.5	5.0	327	1	MOXR_RAT	O9es58 rattus norv
271	91.5	5.2	230	2	Q9YW56	Q9yw56 melanoplus	344	88.5	5.0	344	2	O93242	O93242 gallus gall
272	91.5	5.2	1185	2	Q7PRK4	Q7prk4 anopheles g	345	88.5	5.0	355	2	Q7Q1W7	Q7q1w7 anopheles g
273	91	5.1	308	2	Q68EV1	Q68ev1 xenopus lae	346	88.5	5.0	532	2	Q8WV6	Q8wv6 homo sapien
274	91	5.1	388	2	O8NC34	O8nc34 homo sapien	347	88.5	5.0	534	2	Q96SA2	Q96sa2 homo sapien
275	91	5.1	399	2	Q7QCH7	Q7qch7 anopheles g	348	88.5	5.0	554	2	Q9W4R3	Q9w4r3 drosophila
276	91	5.1	467	2	O8C6F2	O8c6f2 mus musculus	349	88.5	5.0	620	2	O6TGL3	O6tgl3 drosophila
277	91	5.1	467	2	Q91V79	Q91v79 mus musculus	350	88.5	5.0	1081	2	O8T4N8	O8t4n8 penaeus sem
278	91	5.1	491	1	KCS3_RABIT	Q9tt17 myctolagus	351	88.5	5.0	1283	2	O7RQP8	O7rqp8 plasmodium
279	91	5.1	510	2	Q9BGY6	Q9bgy6 macaca fasc	352	88.5	5.0	1390	1	MET_HUMAN	P08581 homo sapien
280	91	5.1	822	1	CAN3_BOVIN	P51186 bos taurus	353	88	5.0	320	2	Q737C6	Q737c6 bacillus ce
281	91	5.1	1150	2	Q6PCX3	Q6pcx3 mus musculus	354	88	5.0	324	2	O7TMH2	O7tmh2 mus musculus
282	91	5.1	1456	2	Q92626	Q92626 homo sapien	355	88	5.0	329	2	Q9TTF2	Q9ttf2 canis famil
283	91	5.1	1548	1	JDID_MOUSE	Q62240 mus musculus	356	88	5.0	337	2	Q9IAZ4	Q9iaza spherooides
284	91	5.1	1840	2	Q9J103	Q9j103 rattus norv	357	88	5.0	339	2	Q9IB09	Q9ib09 spherooides
285	91	5.1	1842	2	O8IZY3	O8izy3 homo sapien	358	88	5.0	343	2	Q8R4Y0	Q8r4y0 mus musculus
286	91	5.1	2053	2	O8IZY4	O8izy4 homo sapien	359	88	5.0	363	1	MURG_BORBU	O51708 borrelia bu
287	91	5.1	2053	2	Q8WU7	Q8wu7 homo sapien	360	88	5.0	419	2	O6P520	O6p520 homo sapien
288	91	5.1	2052	2	Q76MU9	Q76mu9 homo sapien	361	88	5.0	422	2	O58124	O58124 pyrococcus
289	91	5.1	2113	2	Q8TD84	Q8td84 homo sapien	362	88	5.0	457	2	O61396	O61396 mus musculus
290	90.5	5.1	230	2	O8OIW9	O8oiw9 brachydanio	363	88	5.0	508	1	C6D5_DROME	Q9vfp1 drosophila
291	90.5	5.1	243	2	O6IAZ2	O6iaz2 homo sapien	364	88	5.0	509	1	SHS1_RAT	P97710 r protein-t
292	90.5	5.1	306	2	O6IAZ2	O6iaz2 homo sapien	365	88	5.0	530	2	PVR2_MOUSE	P32507 mus musculus
293	90.5	5.1	391	2	Q7TSA3	Q7tsa3 mus musculus	366	88	5.0	530	2	O8OXJ5	Q80xj5 mus musculus
294	90.5	5.1	412	2	Q63611	Q63611 rattus norv	367	88	5.0	623	2	Q7FUC7	Q7fuc7 anopheles g
295	90.5	5.1	412	2	Q9RLE1	Q9rie1 rattus norv	368	88	5.0	639	2	PTPE_MOUSE	Q6pa27 xenopus lae
296	90.5	5.1	417	1	PVR_HUMAN	P15151 homo sapien	369	88	5.0	699	1	PTPE_MOUSE	P49446 mus musculus
297	90.5	5.1	483	2	Q7SX76	Q7sx76 brachydanio	370	88	5.0	699	2	O61042	O61042 mus musculus
298	90.5	5.1	483	2	Q6IR38	O6ir38 mus musculus	371	88	5.0	821	1	CAN3_RAT	P16259 rattus norv
299	90.5	5.1	922	2	Q9LTL7	Q9ltl7 arabisopsis	372	88	5.0	837	2	O8G5I8	O8g5i8 bifidobacte
300	90.5	5.1	1012	1	ROB4_MOUSE	Q8c310 mus musculus	373	88	5.0	986	2	Q8UVR9	Q8uvr9 fugu rubrip
301	90.5	5.1	1905	1	Y659_PASMU	Q9cmz1 pasteurella	374	88	5.0	1092	1	NCA2_XENLA	P36335 xenopus lae
302	90	5.1	250	1	LFA3_HUMAN	P19256 homo sapien	375	88	5.0	1379	2	O8I3S7	Q8i3s7 plasmodium
303	90	5.1	309	2	Q91YV7	Q91yv7 mus musculus	376	88	5.0	1925	1	PXD1_HUMAN	Q9yad7 homo sapien
304	90	5.1	348	1	NEGR_MOUSE	Q80z24 mus musculus	377	88	5.0	3007	2	O142I5	O142i5 homo sapien
305	90	5.1	419	1	PSG1_HUMAN	P11464 homo sapien	378	88	5.0	6669	1	NEBU_HUMAN	P20329 homo sapien
306	90	5.1	541	1	IR18_HUMAN	Q13478 homo sapien	379	87.5	4.9	265	1	CEA7_HUMAN	Q14002 homo sapien
307	90	5.1	609	2	Q9WHH7	Q9whh7 rinderpest	380	87.5	4.9	276	2	Q98822	Q98822 human adeno
308	90	5.1	1179	2	Q7QXR2	Q7qxr2 giardia lam	381	87.5	4.9	276	2	O64861	Q64861 human adeno
309	90	5.1	1290	2	O6WLB5	O6wlb5 chaetopsis	382	87.5	4.9	325	2	O02838	O02838 sus scrofa
310	90	5.1	1431	2	Q8OU60	Q8ou60 mus musculus	383	87.5	4.9	332	2	O640U3	O640u3 xenopus tro
311	89.5	5.1	243	1	CD48_HUMAN	P09326 homo sapien	384	87.5	4.9	403	2	Q8VE47	Q8ve47 mus musculus
312	89.5	5.1	349	1	OMPA_BUCAI	P57414 buchnera ap	385	87.5	4.9	422	1	K3L1_RAT	P83556 rattus norv
313	89.5	5.1	756	2	O8CJW2	Q8cjlw2 streptomyce	386	87.5	4.9	464	2	O6GL25	O6gl25 xenopus tro
314	89.5	5.1	770	2	Q89LN9	Q89ln9 bradyrhizob	387	87.5	4.9	487	2	Q7T2H2	Q7t2h2 gallus gall
315	89.5	5.1	821	1	CAN3_PIG	P43368 sus scrofa	388	87.5	4.9	547	2	O6MG93	O6mg93 rattus norv
316	89.5	5.1	833	2	Q9BPQ7	Q9bpq7 halocynthia	389	87.5	4.9	581	2	Q6EN45	Q6en45 debaryomyce
317	89.5	5.1	845	1	SLK2_HUMAN	Q9hl56 homo sapien	390	87.5	4.9	583	1	C166_MOUSE	Q31192 mus musculus
318	89.5	5.1	845	2	O6A1I3	O6a1i3 homo sapien	391	87.5	4.9	583	1	C166_RAT	O35112 rattus norv
319	89.5	5.1	1024	1	FRM4_HUMAN	Q9p2q2 homo sapien	392	87.5	4.9	652	2	O89703	Q89703 cassava vei
320	89.5	5.1	1644	2	Q9W3D2	Q9w3d2 drosophila	393	87.5	4.9	769	1	PIGR_RAT	P15083 rattus norv
321	89.5	5.1	1671	2	O9W3D3	Q9w3d3 drosophila	394	87.5	4.9	1087	2	Q9PUF6	Q9puf6 gallus gall
322	89.5	5.1	2214	2	O95425	O95425 homo sapien	395	87.5	4.9	2307	2	Q80IV2	Q80iv2 theiler-lik
323	89.5	5.1	3193	2	Q7RLJ38	Q7rlj38 plasmodium	396	87.5	4.9	2340	2	Q78DX7	Q78dx7 mus musculus

397	87.5	4.9	4162	2	Q98918	Q98918 gallus gall	470	85.5	4.8	657	2	Q93D79	Q93d79 bacillus th
398	87.5	4.9	4283	2	Q9ERV0	Q9erv0 rattus norv	471	85.5	4.8	767	2	Q64SV4	Q64sv4 bacteroides
399	87.5	4.9	17903	2	Q7RTL4	Q7rtl4 drosophila	472	85.5	4.8	789	2	Q69270	Q69270 bacillus th
400	87.5	4.9	18074	2	Q917U4	Q9i7u4 drosophila	473	85.5	4.8	789	2	Q938Z1	Q938z1 bacillus th
401	87	4.9	229	2	Q9R121	Q9r121 rattus norv	474	85.5	4.8	789	2	Q45792	Q45792 bacillus th
402	87	4.9	291	2	Q8C191	Q8c191 mus musculu	475	85.5	4.8	789	2	Q45792	Q45792 bacillus th
403	87	4.9	306	2	Q6ZQI3	Q6zqi3 mus musculu	476	85.5	4.8	789	2	Q958G2	Q958g2 bacillus th
404	87	4.9	341	2	Q61353	Q61353 mus musculu	477	85.5	4.8	789	1	KFMS_PSVND	P00545 feline sarc
405	87	4.9	403	2	Q9C6V8	Q9cy68 mus musculu	478	85.5	4.8	1101	2	Q7XDJ5	Q7xdj5 oryza sativ
406	87	4.9	415	2	Q8G6X8	Q8gc68 mus musculu	479	85.5	4.8	1101	2	Q9FWL8	Q9fwl8 oryza sativ
407	87	4.9	457	1	CD4_MOUSE	P06332 mus musculu	480	85.5	4.8	1254	2	Q9VIC7	Q9vic7 drosophila
408	87	4.9	491	1	KCS3_HUMAN	Q9bq31 homo sapien	481	85.5	4.8	1354	2	Q7Q5D1	Q7q5d1 anopheles g
409	87	4.9	491	2	Q8BQZ8	Q8bqz8 mus musculu	482	85.5	4.8	1354	2	Q7Q5D1	Q7q5d1 anopheles g
410	87	4.9	514	2	Q8BH18	Q8bh18 m mus muscu	483	85.5	4.8	1588	2	Q7RQQA	Q7rqqa plasmodium
411	87	4.9	521	1	C166_RABIT	Q46651 oryctolagus	484	85.5	4.8	2115	2	Q8IE55	Q8ie55 plasmodium
412	87	4.9	522	2	Q8F7F1	Q8f7f1 leptospira	485	85.5	4.8	2129	2	Q6FUN0	Q6fun0 candida gla
413	87	4.9	583	1	C166_HUMAN	Q13740 homo sapien	486	85.5	4.8	2491	1	MPRI_HUMAN	P11717 homo sapien
414	87	4.9	609	2	Q7EYK0	Q7eyk0 oryza sativ	487	85.5	4.8	2491	2	Q96PT5	Q96pt5 homo sapien
415	87	4.9	873	2	Q8CD46	Q8cd46 mus musculu	488	85.5	4.8	2491	2	Q7Z7G9	Q7z7g9 homo sapien
416	87	4.9	884	2	Q6NVD0	Q6nvd0 mus musculu	489	85.5	4.8	2588	2	Q88491	Q88491 mus musculu
417	87	4.9	1403	2	Q6DCT7	Q6dct7 xenopus lae	490	85	4.8	2623	2	Q6WRI0	Q6wri0 homo sapien
418	87	4.9	1501	2	Q7TT17	Q7tt17 mus musculu	491	85	4.8	224	2	Q870G0	Q870g0 podospira a
419	87	4.9	1569	2	Q6PAC0	Q6pac0 mus musculu	492	85	4.8	280	2	Q8UWL1	Q8uwl1 ictalurus p
420	87	4.9	1666	1	MYM1_MOUSE	Q62234 mus musculu	493	85	4.8	293	2	Q8WG56	Q8wg56 rattus norv
421	87	4.9	1904	2	Q64699	Q64699 mus musculu	494	85	4.8	332	2	Q75FS2	Q75fs2 leptospira
422	87	4.9	2673	2	Q96SC3	Q96sc3 homo sapien	495	85	4.8	332	2	Q8EXS1	Q8exs1 leptospira
423	87	4.9	3707	1	PGBM_MOUSE	Q05793 mus musculu	496	85	4.8	375	2	Q93GD6	Q93gd6 desulfovibr
424	86.5	4.9	240	2	Q6WG56	Q6mg96 rattus norv	497	85	4.8	379	2	Q8OUL9	Q8oul9 mus musculu
425	86.5	4.9	293	2	Q8AXN8	Q8axn8 cyprinus ca	498	85	4.8	402	1	RAGE_RAT	Q63495 rattus norv
426	86.5	4.9	313	2	Q35531	Q35531 rattus norv	499	85	4.8	402	2	Q8MG86	Q8mg86 rattus norv
427	86.5	4.9	324	2	Q91AY9	Q91ay9 spheeroides	500	85	4.8	428	1	PSG3_HUMAN	Q16557 homo sapien
428	86.5	4.9	443	1	EX7L_VIBVU	Q8df05 vibrio vuln	501	85	4.8	475	2	Q6NZH8	Q6nzh8 xenopus tro
429	86.5	4.9	461	2	Q7MNE3	Q7mne3 vibrio vuln	502	85	4.8	570	2	Q6GLY1	Q6gly1 xenopus lae
430	86.5	4.9	474	2	P79355	P79355 felis silve	503	85	4.8	583	1	C166_BOVIN	Q9bh13 bos taurus
431	86.5	4.9	528	2	Q9RTP5	Q9rtp5 deinococcus	504	85	4.8	684	2	Q21138	Q21138 caenorhadi
432	86.5	4.9	650	2	Q8BEN9	Q8ben9 pseudomonas	505	85	4.8	709	2	Q21138	Q21138 caenorhadi
433	86.5	4.9	711	2	Q6LJAI	Q6ljai photobacter	506	85	4.8	821	1	CAN3_MOUSE	Q64691 mus musculu
434	86.5	4.9	846	1	SLK2_MOUSE	Q810c0 mus musculu	507	85	4.8	875	2	Q91ZY7	Q91zy7 mus musculu
435	86.5	4.9	1028	2	Q61NE5	Q61nb5 xenopus lae	508	85	4.8	880	2	Q6A7L8	Q6a7l8 propionibac
436	86	4.9	259	2	Q9Y5B2	Q9y5b2 homo sapien	509	85	4.8	880	2	Q8AZ23	Q8az23 porcine lym
437	86	4.9	265	2	Q959R3	Q959r3 simian aden	510	85	4.8	1376	2	Q8AZ23	Q8az23 porcine lym
438	86	4.9	280	2	Q8UWK1	Q8uwk1 ictalurus p	511	85	4.8	1384	2	Q769I5	Q769i5 bos taurus
439	86	4.9	330	2	Q6PEU7	Q6peu7 mus musculu	512	85	4.8	1598	2	Q9P214	Q9p214 homo sapien
440	86	4.9	339	2	Q91AZ1	Q91az1 spheeroides	513	84.5	4.8	1723	2	Q8CHB2	Q8chb2 mus musculu
441	86	4.9	348	1	NEGR_RAT	Q9z0i8 rattus norv	514	84.5	4.8	2487	2	Q9N1M0	Q9n1m0 ornithorhyn
442	86	4.9	354	1	VGL1_VZVD	P09258 varicella-z	515	84.5	4.8	238	2	Q749M2	Q749m2 geobacter s
443	86	4.9	354	2	Q98VN1	Q98vni human herpe	516	84.5	4.8	280	2	Q899D0	Q899d0 clostridium
444	86	4.9	354	2	Q775H3	Q775h3 human herpe	517	84.5	4.8	292	1	Y152_HUMAN	Q14165 homo sapien
445	86	4.9	354	2	Q77JF6	Q77jf6 human herpe	518	84.5	4.8	303	2	Q9UKJ1	Q9ukj1 homo sapien
446	86	4.9	354	2	Q77NN4	Q77nn4 human herpe	519	84.5	4.8	337	2	Q6S5Q7	Q6s5q7 mus musculu
447	86	4.9	413	2	Q6ZNI1	Q6zni1 homo sapien	520	84.5	4.8	352	1	NEGR_HUMAN	Q7z3b1 homo sapien
448	86	4.9	428	2	Q9BRW2	Q9brw2 homo sapien	521	84.5	4.8	394	2	Q9D0G8	Q9d0g8 m mus muscu
449	86	4.9	486	2	Q82NI6	Q82ni6 streptomyce	522	84.5	4.8	397	2	Q6XRC3	Q6xrc3 homo sapien
450	86	4.9	487	2	Q82MI3	Q82mi3 streptomyce	523	84.5	4.8	656	2	Q04533	Q04533 arabidopsis
451	86	4.9	545	2	Q9VCT4	Q9vct4 drosophila	524	84.5	4.8	798	2	Q86K66	Q86k66 dictyosteli
452	86	4.9	648	2	Q6DJ24	Q6dj24 xenopus tro	525	84.5	4.8	840	2	Q7VQI2	Q7vqi2 candidatus
453	86	4.9	687	2	Q9MAJ5	Q9maj5 arabidopsis	526	84.5	4.8	1164	2	Q8PX58	Q8px58 methanosarc
454	86	4.9	728	2	Q762C8	Q762c8 homo sapien	527	84.5	4.8	1211	1	M10L_HUMAN	Q8bxt6 homo sapien
455	86	4.9	731	2	Q8SPI6	Q8spi6 macropus eu	528	84	4.7	1608	2	Q8PVI0	Q8pvi0 methanosarc
456	86	4.9	885	1	RFL1_ARATH	Q8sp16 macropus eu	529	84	4.7	4311	2	Q7YQK5	Q7yqk5 canis famil
457	86	4.9	1187	2	Q98TF0	Q98tf0 cyprinus ca	530	84	4.7	262	2	Q9PTR7	Q9ptr7 spheeroides
458	86	4.9	1252	2	Q6CUN8	Q6cun8 kluyveromyc	531	84	4.7	333	2	Q9IB04	Q9ib04 spheeroides
459	86	4.9	1437	2	Q15070	Q15070 homo sapien	532	84	4.7	343	2	Q8BYS4	Q8bys4 mus musculu
460	86	4.9	1812	2	Q7Z261	Q7z261 brachydanio	533	84	4.7	363	2	Q660A8	Q660a8 borrelia ga
461	85.5	4.8	235	2	Q6GXM6	Q6gxm6 homo sapien	534	84	4.7	403	2	Q8ENX5	Q8enx5 oceanobacil
462	85.5	4.8	249	2	Q6XJV6	Q6xjv6 mus musculu	535	84	4.7	457	2	Q8FAG8	Q8fag8 acinetobact
463	85.5	4.8	324	2	Q9UPK8	Q9upk8 homo sapien	536	84	4.7	509	2	Q6P6I8	Q6p6i8 mus musculu
464	85.5	4.8	326	2	Q9UPK8	Q9upk8 homo sapien	537	84	4.7	556	2	Q7ZZU8	Q7zzu8 brachydanio
465	85.5	4.8	333	2	Q75237	Q75237 homo sapien	538	84	4.7	593	2	Q8NKB1	Q8nkb1 emericella
466	85.5	4.8	395	2	Q75237	Q75237 homo sapien	539	84	4.7	611	2	Q73TM4	Q73tm4 mycobacteri
467	85.5	4.8	393	2	Q7TNZ6	Q7tnz6 rattus norv	540	84	4.7	668	1	PBS2_YEAST	P08018 saccharomyc
468	85.5	4.8	527	2	Q6YW20	Q6yw20 oryza sativ	541	84	4.7	775	2	Q97754	Q97754 oryctolagus
469	85.5	4.8	650	2	Q8NA84	Q8na84 homo sapien	542	84	4.7	800	2	Q8H329	Q8h329 oryza sativ
										811	2	Q8T3J2	Q8t3j2 drosophila
										811	2	Q9VK54	Q9vk54 drosophila

543	84	4.7	812	2	Q8M257	Q8m257 drosophila	616	83	4.7	2489	2	Q06116	Q06116 saccharomyc
544	84	4.7	851	2	Q9UX76	Q9ux76 sulfolobus	617	82.5	4.7	155	2	Q06P81	Q06p81 homo sapien
545	84	4.7	880	2	P91643	P91643 drosophila	618	82.5	4.7	230	2	Q8UV76	Q8uv76 brachydanio
546	84	4.7	1028	2	Q7XTIP5	Q7xtip5 oryza sativ	619	82.5	4.7	244	2	Q7YS40	Q7ys40 sus scrofa
547	84	4.7	1062	2	Q997A4	Q997a4 american pl	620	82.5	4.7	319	1	A33 MOUSE	Q9jka5 mus musculus
548	84	4.7	1098	2	Q6FXS8	Q6fxs8 candida gla	621	82.5	4.7	330	2	P97269	P97269 cavia porce
549	84	4.7	1193	2	Q9VQW1	Q9vqw1 drosophila	622	82.5	4.7	373	2	Q9SSH0	Q9ssh0 arabidopsis
550	84	4.7	1300	1	IRR MOUSE	Q9wt14 mus musculus	623	82.5	4.7	378	2	Q8LY42	Q8ly42 arabidopsis
551	84	4.7	1379	1	MET MOUSE	P16056 mus musculus	624	82.5	4.7	382	2	Q6VEU7	Q6veu7 mus musculus
552	84	4.7	1499	2	Q90815	Q90815 gallus gall	625	82.5	4.7	393	2	Q9C9P8	Q9c9p8 arabidopsis
553	84	4.7	3034	1	CLRI MOUSE	Q35161 mus musculus	626	82.5	4.7	446	2	Q8NK03	Q8nk03 emericeila
554	83.5	4.7	210	2	Q7PVL9	Q7pvl9 anopheles g	627	82.5	4.7	468	2	Q6PJ50	Q6pj50 mus musculus
555	83.5	4.7	289	2	Q9GLJ33	Q9glj33 bos taurus	628	82.5	4.7	576	2	Q8TK0K	Q8tk0k methanosarc
556	83.5	4.7	289	2	Q8K3J3	Q8k3j3 meriones un	629	82.5	4.7	600	2	Q7PN36	Q7pn36 anopheles g
557	83.5	4.7	298	1	JAM2 HUMAN	P57087 homo sapien	630	82.5	4.7	773	1	MES2 CAEEL	Q17514 caenorhabdi
558	83.5	4.7	298	2	Q6YNC1	Q6ync1 homo sapien	631	82.5	4.7	833	2	Q9VHG1	Q9vng1 drosophila
559	83.5	4.7	306	2	Q6PYW4	Q6pyw4 schistosoma	632	82.5	4.7	840	2	Q84BZ6	Q84bz6 spiroplasma
560	83.5	4.7	312	2	Q6UXG6	Q6uxg6 homo sapien	633	82.5	4.7	840	2	Q84BZ7	Q84bz7 spiroplasma
561	83.5	4.7	315	2	O5U082	O5u082 pyrococcus	634	82.5	4.7	986	2	Q6DG17	Q6dg17 brachydanio
562	83.5	4.7	391	2	Q6P5F0	Q6pf5f0 mus musculus	635	82.5	4.7	994	2	Q96167	Q96167 plasmodium
563	83.5	4.7	392	2	Q76708	Q76708 caenorhabdi	636	82.5	4.7	1028	2	Q90Q52	Q90q52 homo sapien
564	83.5	4.7	408	2	Q8K094	Q8k094 m hypochoeti	637	82.5	4.7	1241	2	Q83GQ1	Q83gq1 tropheryma
565	83.5	4.7	408	2	Q91WP1	Q91wp1 mus musculus	638	82.5	4.7	1319	2	Q9BJF3	Q9bjf3 oxytricha t
566	83.5	4.7	408	2	Q8BYF6	Q8byf6 mus musculus	639	82.5	4.7	1567	2	Q6MIA1	Q6mia1 bdellovibri
567	83.5	4.7	450	2	Q6UXI0	Q6uxi0 homo sapien	640	82.5	4.7	2597	2	Q6WRH9	Q6wrh9 rattus norv
568	83.5	4.7	515	2	Q66PJ5	Q66pj5 homo sapien	641	82.5	4.7	3100	2	Q7KYN5	Q7kyn5 homo sapien
569	83.5	4.7	515	2	Q96RE0	Q96re0 homo sapien	642	82.5	4.7	4034	2	Q6ZX14	Q6zx14 magnaportha
570	83.5	4.7	528	2	P91670	P91670 drosophila	643	82.5	4.7	4256	2	Q8WJF3	Q8wjf3 canis famli
571	83.5	4.7	577	2	Q8IH34	Q8ih34 bacillus ce	644	82.5	4.7	4650	2	Q15598	Q15598 homo sapien
572	83.5	4.7	580	2	Q6C7F7	Q6c7f7 yarowia li	645	82.5	4.7	26926	2	Q10466	Q10466 homo sapien
573	83.5	4.7	646	2	Q899Y4	Q899y4 clostridium	646	82.5	4.7	26926	2	Q8WZB3	Q8wzb3 homo sapien
574	83.5	4.7	1059	2	Q9DE49	Q9de49 brachydanio	647	82.5	4.7	34350	2	Q8WZ42	Q8wz42 homo sapien
575	83.5	4.7	1160	2	Q6G587	Q6g587 bartonella	648	82.5	4.7	151	2	Q7YS88	Q7ys88 sus scrofa
576	83.5	4.7	1332	2	Q6F5X7	Q6f5x7 candida gla	649	82	4.6	184	2	Q7VM71	Q7vm71 haemophilus
577	83.5	4.7	1463	2	O55124	O55124 mus musculus	650	82	4.6	308	2	Q95K99	Q95k99 macaca fasc
578	83.5	4.7	1501	2	Q9QW00	Q9qw00 rattus sp.	651	82	4.6	324	2	Q8NBY8	Q8nby8 homo sapien
579	83.5	4.7	1556	2	Q83NF7	Q83nf7 tropheryma	652	82	4.6	326	2	Q8NC17	Q8nc17 homo sapien
580	83.5	4.7	1802	2	Q9J5C2	Q9j5c2 fowlpox vir	653	82	4.6	327	2	Q96IQ7	Q96iq7 homo sapien
581	83.5	4.7	1863	2	Q64605	Q64605 rattus norv	654	82	4.6	331	2	Q91B01	Q91b01 spherooides
582	83.5	4.7	3354	2	Q7PL03	Q7pl03 anopheles g	655	82	4.6	386	1	NATB BACSU	P46304 bacillus su
583	83.5	4.7	4651	2	Q7PL01	Q7pl01 anopheles g	656	82	4.6	409	2	Q814M1	Q814m1 bacillus ce
584	83	4.7	151	2	Q7YS89	Q7ys89 sus scrofa	657	82	4.6	412	2	Q8HY14	Q8hy14 cryctolagus
585	83	4.7	231	2	Q8WYV6	Q8wyv6 homo sapien	658	82	4.6	444	2	Q8S917	Q8s917 arabidopsis
586	83	4.7	234	2	Q78T27	Q78t27 mus musculus	659	82	4.6	449	2	P78721	P78721 orpinomyces
587	83	4.7	237	2	Q6DOX5	Q6d0x5 cryctolagus	660	82	4.6	587	2	Q91AA1	Q91aa1 carassius a
588	83	4.7	261	2	Q7M5H2	Q7m5h2 fowl adenov	661	82	4.6	609	1	HEMA RINDR	P41355 rinderpest
589	83	4.7	281	2	Q8CJEB8	Q8cje8 mesocricetu	662	82	4.6	609	2	Q6LAC4	Q6lac4 rinderpest
590	83	4.7	305	2	Q6ZS95	Q6zs95 homo sapien	663	82	4.6	634	2	Q9P8L1	Q9p8l1 cryptococcu
591	83	4.7	339	2	Q91AZ2	Q91az2 spherooides	664	82	4.6	636	2	Q64VT4	Q64vt4 bacteroides
592	83	4.7	369	2	Q93EW5	Q93ew5 desulfovibr	665	82	4.6	648	2	Q9EPF1	Q9epf1 mus musculus
593	83	4.7	373	2	Q8TU74	Q8tu74 methanosarc	666	82	4.6	709	2	Q9XSJ1	Q9xsj1 bos taurus
594	83	4.7	401	2	Q98835	Q98835 cercopithe	667	82	4.6	737	2	O08702	O08702 rattus norv
595	83	4.7	420	2	Q68DM9	Q68dm9 homo sapien	668	82	4.6	737	2	O70376	O70376 rattus norv
596	83	4.7	424	2	Q6CLK2	Q6clk2 klyveromyc	669	82	4.6	757	2	O70482	O70482 rattus norv
597	83	4.7	437	2	Q90W14	Q90w14 gallus gall	670	82	4.6	785	2	Q9QZF9	Q9qzf9 rattus norv
598	83	4.7	448	2	Q6LU33	Q6lu33 photobacter	671	82	4.6	880	1	TYO3 MOUSE	P55144 mus musculus
599	83	4.7	463	1	STRA_PSEFL	O05139 pseudomonas	672	82	4.6	880	2	Q6NZM6	Q6nzm6 mus musculus
600	83	4.7	514	2	Q9HOC3	Q9hoc3 homo sapien	673	82	4.6	1007	1	GRD2 HUMAN	O43424 homo sapien
601	83	4.7	538	2	Q9DFU0	Q9dfu0 sparus aura	674	82	4.6	1038	2	Q8CHA3	Q8cha3 mus musculus
602	83	4.7	577	2	Q9D2Z1	Q9d2z1 m mus muscu	675	82	4.6	1166	2	Q8OVPO	Q8ovp0 mus musculus
603	83	4.7	594	2	Q64NY2	Q64ny2 bacteroides	676	82	4.6	1358	2	Q6PA47	Q6pa47 xenopus lae
604	83	4.7	757	1	PIGR BOVIN	P81265 bos taurus	677	82	4.6	2036	1	GRIP HUMAN	Q6gyq0 homo sapien
605	83	4.7	873	1	LDVR_HUMAN	P98155 homo sapien	678	82	4.6	2136	2	Q8RYW8	Q8ryw8 oryza sativ
606	83	4.7	873	2	Q6S4M1	Q6s4m1 macaca mula	679	82	4.6	2940	2	Q8IHP9	Q8ihp9 plasmodium
607	83	4.7	925	2	O44191	O44191 caenorhabdi	680	82	4.6	3173	2	Q882M6	Q882m6 pseudomonas
608	83	4.7	925	2	Q9U4E4	Q9u4e4 caenorhabdi	681	82	4.6	3562	1	PGCV CHICK	Q90953 gallus gall
609	83	4.7	925	2	Q9UB94	Q9ub94 caenorhabdi	682	82	4.6	5636	2	Q96RW7	Q96rw7 homo sapien
610	83	4.7	925	2	Q9UB95	Q9ub95 caenorhabdi	683	81.5	4.6	206	2	Q6WIR9	Q6wir9 aspergillus
611	83	4.7	1106	1	ACLY CAEEL	P53585 caenorhabdi	684	81.5	4.6	236	2	Q6P5S3	Q6p5s3 homo sapien
612	83	4.7	1106	2	Q8IBR5	Q8ibr5 plasmodium	685	81.5	4.6	275	2	Q8AVV1	Q8avv1 xenopus lae
613	83	4.7	1254	2	Q674V1	Q674v1 podocoryne	686	81.5	4.6	301	1	OX2G RAT	P04218 rattus norv
614	83	4.7	1382	2	Q64GK4	Q64gk4 brachydanio	687	81.5	4.6	478	2	Q7Q864	Q7q864 anopheles g
615	83	4.7	2421	2	Q95MJ1	Q95mj1 lemur catta	688	81.5	4.6	302	1	ICOL_HUMAN	O75144 homo sapien

689	81.5	4.6	329	2	Q91AY6	Q91ay6 spherooides	762	81	4.6	937	2	Q8G4P3	Q8g4p3 bifidobacte
690	81.5	4.6	336	2	Q90Z89	Q90z89 brachydanio	763	81	4.6	1079	2	Q8E7G6	Q8e7g6 canis famil
691	81.5	4.6	340	2	Q90IAZ6	Q90iaz6 spherooides	764	81	4.6	1196	2	Q8E7F1	Q8e7f1 cyrinus ca
692	81.5	4.6	350	2	Q6RJN1	Q6rjn1 homo sapien	765	81	4.6	1220	2	Q8P3A8	Q8p3a8 schizosacch
693	81.5	4.6	352	2	Q08Z66	Q08z66 homo sapien	766	81	4.6	1304	1	NRCA_HUMAN	Q92823 homo sapien
694	81.5	4.6	352	2	Q15403	Q15403 homo sapien	767	81	4.6	1305	2	Q6ZPE0	Q6zpe0 mus musculu
695	81.5	4.6	355	2	Q65493	Q65493 arabidopsis	768	81	4.6	1898	2	Q64604	Q64604 r proteoin-t
696	81.5	4.6	373	2	Q65493	Q65493 arabidopsis	769	81	4.6	1901	2	Q7UI70	Q7ui70 rhodopirell
697	81.5	4.6	378	1	LEUK_RAT	P13838 rattus norv	770	81	4.6	2219	2	Q88W19	Q88w19 lactobacill
698	81.5	4.6	402	2	Q6ZG94	Q6zg94 oryza sativ	771	81	4.6	2402	2	Q9AER7	Q9aer7 staphylococ
699	81.5	4.6	411	2	Q15228	Q15228 homo sapien	772	80.5	4.5	261	2	Q9W6V1	Q9w6v1 gallus gall
700	81.5	4.6	438	2	Q7T0Z8	Q7t0z8 xenopus lae	773	80.5	4.5	290	2	Q8CRR9	Q8crr9 staphylococ
701	81.5	4.6	440	2	Q6ZMD4	Q6zmd4 homo sapien	774	80.5	4.5	346	1	EPB1_HUMAN	P98172 homo sapien
702	81.5	4.6	444	2	Q6K2Y8	Q6k2y8 oryza sativ	775	80.5	4.5	371	2	Q633A8	Q633a8 bacillus ce
703	81.5	4.6	473	2	Q8ZQD1	Q8zqd1 salmonella	776	80.5	4.5	371	2	Q72Z49	Q72z49 bacillus ce
704	81.5	4.6	479	2	Q6GNX2	Q6gnx2 xenopus lae	777	80.5	4.5	371	2	Q816Y2	Q816y2 bacillus ce
705	81.5	4.6	493	2	Q6CGB7	Q6cgb7 yarrowia li	778	80.5	4.5	371	2	Q6HCJ8	Q6hcj8 bacillus th
706	81.5	4.6	497	1	GAUT_CLOAB	Q976z4 clostridium	779	80.5	4.5	376	1	GCF1_ARATH	Q94b08 arabidopsis
707	81.5	4.6	502	2	Q84ZD1	Q84zd1 escherichia	780	80.5	4.5	388	2	Q8R464	Q8r464 mus musculu
708	81.5	4.6	504	2	Q8N441	Q8n441 homo sapien	781	80.5	4.5	462	1	MURD_CLOAB	Q97eb9 clostridium
709	81.5	4.6	504	2	Q9H4D7	Q9h4d7 homo sapien	782	80.5	4.5	472	2	Q811T8	Q811t8 mus musculu
710	81.5	4.6	507	2	Q751G2	Q751g2 ashbya goss	783	80.5	4.5	473	2	Q8Z809	Q8z809 salmonella
711	81.5	4.6	522	2	Q64DK4	Q64dk4 uncultured	784	80.5	4.5	475	2	Q6Z056	Q6z056 mus musculu
712	81.5	4.6	524	2	Q09012	Q09012 shigella so	785	80.5	4.5	476	1	YCAM_ECOLI	P75835 escherichia
713	81.5	4.6	524	2	Q75SW4	Q75sw4 escherichia	786	80.5	4.5	498	2	Q886D9	Q886d9 pseudomonas
714	81.5	4.6	525	2	Q6VMU4	Q6vmu4 escherichia	787	80.5	4.5	540	2	Q8XEB5	Q8xeb5 escherichia
715	81.5	4.6	525	2	Q6VMU5	Q6vmu5 escherichia	788	80.5	4.5	546	2	Q8OX70	Q8ox70 mus musculu
716	81.5	4.6	525	2	Q6VMU6	Q6vmu6 escherichia	789	80.5	4.5	548	2	Q99NB3	Q99nb3 mus musculu
717	81.5	4.6	606	2	Q9VNN6	Q9vnn6 drosophila	790	80.5	4.5	556	2	Q8DEW4	Q8dew4 vibrio vuln
718	81.5	4.6	677	2	Q8A3Q5	Q8a3q5 bacteroides	791	80.5	4.5	564	2	Q7ZU00	Q7zu00 brachydanio
719	81.5	4.6	708	2	Q9W1P4	Q9w1p4 arabidopsis	792	80.5	4.5	602	2	Q86YJ9	Q86yj9 homo sapien
720	81.5	4.6	709	1	Y939_SULTO	Q973g3 sulfolobus	793	80.5	4.5	662	2	Q6O926	Q6o926 homo sapien
721	81.5	4.6	746	2	Q6DIR2	Q6dir2 xenopus tro	794	80.5	4.5	707	2	Q7XNT7	Q7xnt7 oryza sativ
722	81.5	4.6	779	2	Q8AAG1	Q8aag1 bacteroides	795	80.5	4.5	721	1	DPX5_ASPTU	Q13479 aspergillus
723	81.5	4.6	815	1	CAN3_MACFA	Q9gl97 macaca fasc	796	80.5	4.5	739	2	Q865F2	Q865f2 oryctolagus
724	81.5	4.6	824	2	Q8A3C4	Q8a3c4 bacteroides	797	80.5	4.5	789	2	Q8RSZ5	Q8rsz5 bacillus th
725	81.5	4.6	873	2	Q42595	Q42595 xenopus lae	798	80.5	4.5	823	2	Q39594	Q39594 chlamydomon
726	81.5	4.6	925	1	W70T_HUMAN	P57737 homo sapien	799	80.5	4.5	932	2	Q7TQ14	Q7tq14 rattus norv
727	81.5	4.6	968	2	Q9VR40	Q9vr40 drosophila	800	80.5	4.5	976	2	Q8JFR5	Q8jfr5 brachydanio
728	81.5	4.6	1187	2	Q93284	Q93284 fugu rubrip	801	80.5	4.5	976	2	Q9W755	Q9w755 brachydanio
729	81.5	4.6	1194	2	Q93962	Q93962 glomus vers	802	80.5	4.5	1293	2	Q6WLA9	Q6wla9 heterotomu
730	81.5	4.6	1194	2	Q7TFV3	Q7tfv3 mus musculu	803	80.5	4.5	1364	1	BLM_XENLA	Q9dey9 xenopus lae
731	81.5	4.6	1214	2	Q75054	Q75054 homo sapien	804	80.5	4.5	1465	2	Q7Z3Y2	Q7z3y2 homo sapien
732	81.5	4.6	1214	2	Q6ZQA6	Q6zqa6 mus musculu	805	80.5	4.5	1677	2	Q6UAQ6	Q6uaq6 ctenopharyn
733	81.5	4.6	1596	2	Q9HCL6	Q9hcl6 homo sapien	806	80.5	4.5	1948	1	PTNS_HUMAN	Q13332 homo sapien
734	81.5	4.6	212	2	Q8NEN3	Q8nen3 homo sapien	807	80.5	4.5	2253	2	Q8JVZ0	Q8jvz0 ljunjan vir
735	81.5	4.6	284	2	Q815Y7	Q815y7 plaemodium	808	80.5	4.5	2358	2	Q95M02	Q95mj2 macropus ru
736	81.5	4.6	620	2	Q96AA2	Q96aa2 homo sapien	809	80.5	4.5	2898	2	Q872P1	Q872p1 neurospora
737	81	4.6	149	2	Q86L22	Q86l22 dictyosteli	810	80.5	4.5	3337	2	Q9TWY4	Q9twy4 caenorhabdi
738	81	4.6	151	2	Q867B8	Q867b8 sus scrofa	811	80.5	4.5	3343	1	CAD3_CAEL	P34616 caenorhabdi
739	81	4.6	252	2	Q95781	Q95781 homo sapien	812	80.5	4.5	3354	1	CADN_MOUSE	Q99pf4 mus musculu
740	81	4.6	266	2	Q6AYP8	Q6ayp8 rattus norv	813	80.5	4.5	3358	1	PGCV_MOUSE	Q62059 mus musculu
741	81	4.6	272	2	Q861J5	Q861j5 equus cabal	814	80.5	4.5	6632	1	UN89_CAEL	Q01761 caenorhabdi
742	81	4.6	291	2	Q8CD40	Q8cd40 mus musculu	815	80.5	4.5	8081	2	Q7Z120	Q7z120 caenorhabdi
743	81	4.6	326	2	Q91AY7	Q91ay7 spherooides	816	80	4.5	184	2	Q8WVI8	Q8wvi8 homo sapien
744	81	4.6	330	2	Q87W83	Q87w83 pseudomonas	817	80	4.5	227	2	Q9UKJ0	Q9ukj0 homo sapien
745	81	4.6	338	1	LAMP_HUMAN	Q13449 homo sapien	818	80	4.5	235	2	Q99M11	Q99m11 mus musculu
746	81	4.6	374	2	Q43741	Q43741 bromheadia	819	80	4.5	276	2	Q640S5	Q640s5 xenopus tro
747	81	4.6	413	2	Q7QBV1	Q7qbv1 anopheles g	820	80	4.5	303	2	Q7T114	Q7t114 brachydanio
748	81	4.6	413	2	Q7QBV2	Q7qbv2 anopheles g	821	80	4.5	337	2	Q8UV29	Q8uv29 brachydanio
749	81	4.6	423	2	Q9UAG6	Q9uag6 dictyosteli	822	80	4.5	338	1	LAMP_RAT	Q62813 rattus norv
750	81	4.6	438	2	Q920C3	Q920c3 mus musculu	823	80	4.5	341	1	K2L3_HUMAN	P43628 h killer ce
751	81	4.6	451	2	Q8DDA0	Q8dda0 vibrio vuln	824	80	4.5	341	1	LAMP_MOUSE	Q8blk3 mus musculu
752	81	4.6	489	1	C302_DROME	Q9ngx9 drosophila	825	80	4.5	343	2	Q8X5J1	Q8x5j1 escherichia
753	81	4.6	507	2	Q9U319	Q9u319 caenorhabdi	826	80	4.5	365	2	Q8AXL6	Q8axl6 oncorhynch
754	81	4.6	521	1	C166_CANFA	Q46634 canis famil	827	80	4.5	378	2	Q66MN4	Q66mn4 petromyzon
755	81	4.6	624	2	Q94AX9	Q94ax9 arabidopsis	828	80	4.5	436	2	Q99563	Q99563 macaca mula
756	81	4.6	643	2	Q7Y231	Q7y231 arabidopsis	829	80	4.5	440	2	Q8WK36	Q8mk36 pseudobacte
757	81	4.6	648	2	Q6NLT5	Q6ntl5 xenopus lae	830	80	4.5	465	2	Q67TE8	P18275 symbiobacte
758	81	4.6	745	2	Q6NNX7	Q6nnx7 drosophila	831	80	4.5	482	1	ARCD_PSEAE	P18275 pseudomonas
759	81	4.6	760	1	YCBS_YEAST	P25574 saccharomyc	832	80	4.5	492	2	Q8UEG2	Q8ueg2 aspergillus
760	81	4.6	769	2	Q97TIS9	Q97tis9 clostridium	833	80	4.5	509	2	Q920C2	Q920c2 mus musculu
761	81	4.6	829	1	CAD3_HUMAN	P22223 homo sapien	834	80	4.5	516	2	Q81WX2	Q81wx2 homo sapien



835	80	4.5	529	2	Q91V87	Q91V87 mus musculus	908	79	4.5	323	2	Q8NDD2	Q8ndd2 homo sapien
836	80	4.5	535	2	Q65J12	Q65j12 bacillus li	909	79	4.5	340	2	Q6PKA9	Q6pkA9 mus musculus
837	80	4.5	624	2	Q8LG08	Q8lg08 arabidopsis	910	79	4.5	342	2	Q8MK29	Q8mk29 macaca mula
838	80	4.5	627	2	Q9VOL0	Q9vol0 drosophila	911	79	4.5	406	2	Q8BPP7	Q8bPP7 mus musculus
839	80	4.5	633	2	Q78XC1	Q78xc1 brachydanio	912	79	4.5	410	2	Q8BJP5	Q8bjP5 bacillus an
840	80	4.5	637	2	Q9P8P2	Q9p8P2 cryptococcus	913	79	4.5	412	2	Q6MZS4	Q6mZs4 homo sapien
841	80	4.5	681	2	Q75JX7	Q75jx7 dictyosteli	914	79	4.5	429	2	Q8BFS1	Q8bFs1 m mus muscu
842	80	4.5	865	2	Q68DA2	Q68da2 homo sapien	915	79	4.5	438	1	Y232_METJA	Q60289 methanococc
843	80	4.5	902	1	XPF_CRIGR	Q9qyM7 cricetus	916	79	4.5	440	2	Q8MK37	Q8mk37 macaca mula
844	80	4.5	957	2	Q64IF3	Q64if3 xenopus lae	917	79	4.5	446	2	P79762	P79762 gallus gall
845	80	4.5	960	2	Q6BXD5	Q6bxD5 debaryomyce	918	79	4.5	446	2	P79762	P79762 gallus gall
846	80	4.5	1005	2	P79921	P79921 xenopus lae	919	79	4.5	451	2	Q7MQE3	Q7mqE3 vibrio vuln
847	80	4.5	1040	1	AXO1_HUMAN	Q02246 homo sapien	920	79	4.5	463	1	STHA_PSEPK	Q88Kv8 pseudomonas
848	80	4.5	1170	1	TSOL_MOUSE	P35441 mus musculus	921	79	4.5	479	2	Q9K6X5	Q9k6X5 bacillus ha
849	80	4.5	1192	2	Q81Y28	Q81y28 bacillus an	922	79	4.5	490	2	Q6PL22	Q6pl22 homo sapien
850	80	4.5	1310	2	Q81W14	Q81w14 caenorhabdi	923	79	4.5	491	2	Q8GZP5	Q8gzP5 lycopersico
851	80	4.5	1431	2	Q8EW23	Q8ew23 mycoplasma	924	79	4.5	492	2	Q8WU21	Q8wu21 homo sapien
852	80	4.5	1925	2	Q9YRB3	Q9yrb3 nudaurelia	925	79	4.5	517	2	Q76021	Q76021 homo sapien
853	80	4.5	2195	2	Q723M7	Q723m7 listeria mo	926	79	4.5	524	2	Q8LTK1	Q8ltk1 lactococcus
854	80	4.5	2456	2	Q817I5	Q817i5 caenorhabdi	927	79	4.5	526	2	Q8QWA6	Q8Qwa6 mus musculus
855	80	4.5	3064	2	Q8UDW7	Q8udW7 plasmodium	928	79	4.5	584	2	Q9Y3Y8	Q9y3Y8 homo sapien
856	80	4.5	5229	2	Q7RTF4	Q7rtf4 plasmodium	929	79	4.5	590	2	Q9P4U4	Q9p4U4 candida tro
857	79.5	4.5	151	2	Q8C2T1	Q8c2t1 mus musculus	930	79	4.5	611	2	Q9PTI0	Q9ptI0 xenopus lae
858	79.5	4.5	236	2	Q6PIQ7	Q6piq7 homo sapien	931	79	4.5	611	2	Q9PTI0	Q9ptI0 xenopus lae
859	79.5	4.5	237	2	Q6DHW4	Q6dhw4 homo sapien	932	79	4.5	619	2	Q9ASG9	Q9asg9 oryza sativ
860	79.5	4.5	244	2	Q8SQB6	Q8sqb6 sus scrofa	933	79	4.5	644	2	Q66IN5	Q66in5 xenopus lae
861	79.5	4.5	249	1	MYFO_CHICK	P37301 gallus gall	934	79	4.5	657	2	P73359	P73359 synchocyst
862	79.5	4.5	289	2	Q97XZ7	Q97xz7 sulfobolus	935	79	4.5	711	2	Q80Y89	Q80y89 mus musculus
863	79.5	4.5	328	1	CYS4_BRANA	P25251 brassica na	936	79	4.5	778	2	Q9N4B1	Q9n4B1 caenorhabdi
864	79.5	4.5	345	2	Q6GM08	Q6gm08 xenopus lae	937	79	4.5	805	2	Q7TNP4	Q7tnP4 mus musculus
865	79.5	4.5	399	2	Q8EMW2	Q8emW2 oceanobacil	938	79	4.5	857	2	Q8PTE2	Q8pte2 methanosaer
866	79.5	4.5	400	2	Q66E26	Q66e26 yersinia ps	939	79	4.5	853	2	Q19372	Q19372 caenorhabdi
867	79.5	4.5	401	2	Q8ZHN7	Q8zhn7 yersinia pe	940	79	4.5	917	2	Q767M4	Q767m4 sus scrofa
868	79.5	4.5	401	2	Q93534	Q93534 xenopus lae	941	79	4.5	977	2	Q8GZA0	Q8gza0 arabidopsis
869	79.5	4.5	418	2	Q7RL88	Q7rl88 plasmodium	942	79	4.5	996	2	Q6BM64	Q6bm64 debaryomyce
870	79.5	4.5	430	1	TPSN_CHICK	Q73895 gallus gall	943	79	4.5	1030	2	Q7XTP4	Q7xtp4 oryza sativ
871	79.5	4.5	430	2	Q76LJ8	Q76lj8 coturnix co	944	79	4.5	1104	2	Q9FKR7	Q9fkr7 arabidopsis
872	79.5	4.5	446	2	Q69885	Q69885 streptomyce	945	79	4.5	1177	2	Q6QGB1	Q6qgb1 xenopus lae
873	79.5	4.5	474	2	Q7ZU39	Q7zu39 brachydanio	946	79	4.5	1228	1	ALAS_ARATH	Q99gb3 arabidopsis
874	79.5	4.5	490	1	TLME_ECOLI	Q47282 escherichia	947	79	4.5	1264	2	P91767	P91767 manduca sex
875	79.5	4.5	520	2	Q8GDL8	Q8gdl8 photorhabdu	948	79	4.5	1361	1	GLI4_XENLA	Q7xtp4 oryza sativ
876	79.5	4.5	641	2	Q86SD2	Q86sd2 ciona intes	949	79	4.5	1382	2	Q75ZY9	Q75zy9 canis fami
877	79.5	4.5	686	2	Q75WK5	Q75wk5 oryzias lat	950	79	4.5	1390	2	Q7ERL3	Q7err3 plasmodium
878	79.5	4.5	740	1	PECL_PIG	Q95242 sus scrofa	951	79	4.5	1746	2	Q6ZQ83	Q6zq83 mus musculus
879	79.5	4.5	743	2	Q6P4H5	Q6p4H5 homo sapien	952	79	4.5	1887	2	Q9QM67	Q9qM67 rattus sp.
880	79.5	4.5	821	2	Q8C756	Q8c756 mus musculus	953	79	4.5	1925	2	Q68HV1	Q68hv1 mus musculus
881	79.5	4.5	845	2	Q91YV0	Q91yv0 mus musculus	954	79	4.5	4010	1	FRS1_MOUSE	Q80c14 mus musculus
882	79.5	4.5	859	1	PMS2_MOUSE	P54279 mus musculus	955	78.5	4.4	300	1	CEAL_HUMAN	Q7ze92 homo sapien
883	79.5	4.5	873	1	LDVR_MOUSE	P98156 mus musculus	956	78.5	4.4	305	1	PEXQ_MACFA	Q9be65 macaca fasc
884	79.5	4.5	924	2	Q73L80	Q73l80 treponema d	957	78.5	4.4	318	2	Q91664	Q91664 xenopus lae
885	79.5	4.5	961	1	ROB4_RAT	Q80w87 rattus norv	958	78.5	4.4	333	2	Q7MR78	Q7mr78 wolinnella s
886	79.5	4.5	980	1	KFMS_FELCA	P13369 felis silve	959	78.5	4.4	381	2	Q753P2	Q753p2 ashbya goas
887	79.5	4.5	1043	2	Q6PA07	Q6pa07 xenopus lae	960	78.5	4.4	388	2	Q8NfZ8	Q8nfz8 homo sapien
888	79.5	4.5	1162	2	Q75921	Q75921 homo sapien	961	78.5	4.4	392	2	Q7PSN2	Q7psn2 anopheles g
889	79.5	4.5	1162	2	Q9UNY4	Q9uny4 homo sapien	962	78.5	4.4	429	1	EPC_RAT	P01855 rattus norv
890	79.5	4.5	1171	2	Q80YQ1	Q80yq1 mus musculus	963	78.5	4.4	431	2	Q8X022	Q8x022 neurospora
891	79.5	4.5	1171	2	Q8CCB2	Q8ccb2 mus musculus	964	78.5	4.4	452	2	Q76773	Q76773 lucilia cup
892	79.5	4.5	1342	2	Q9GPP6	Q9gpp6 drosophila	965	78.5	4.4	459	2	Q9SS39	Q9ssa39 arabidopsis
893	79.5	4.5	1342	1	Q9VPZ7	Q9vpz7 drosophila	966	78.5	4.4	467	1	SIL5_MOUSE	Q91y57 mus musculus
894	79.5	4.5	1465	1	MYM2_HUMAN	P54296 homo sapien	967	78.5	4.4	471	1	Q9DAV5	Q9dav5 mus musculus
895	79.5	4.5	1614	2	Q7RN98	Q7rn98 plasmodium	968	78.5	4.4	497	1	UBID_ECO57	P58194 escherichia
896	79.5	4.5	1670	2	Q7QZP4	Q7qzp4 giardia lam	969	78.5	4.4	537	2	Q93E12	Q93e12 rhizobium l
897	79.5	4.5	1838	2	Q8B207	Q8b207 mus musculus	970	78.5	4.4	539	2	O04252	O04252 arabidopsis
898	79.5	4.5	2253	2	Q8JUV1	Q8jv21 ljunjan vir	971	78.5	4.4	542	2	Q6PAE8	Q6paE8 xenopus lae
899	79.5	4.5	2256	2	Q8JUV19	Q8jv19 ljunjan vir	972	78.5	4.4	544	2	Q6UXI8	Q6uxi8 homo sapien
900	79.5	4.5	2658	2	Q9GRL9	Q9grl9 leishmania	973	78.5	4.4	556	2	Q8L6Z9	Q8l6z9 arabidopsis
901	79.5	4.5	2706	2	Q97292	Q97292 plasmodium	974	78.5	4.4	591	2	Q6NSU9	Q6nsu9 mus musculus
902	79	4.5	158	2	Q15229	Q15229 homo sapien	975	78.5	4.4	603	2	Q7S314	Q7s314 neurospora
903	79	4.5	210	2	Q9AC09	Q9ac09 caulobacter	976	78.5	4.4	628	1	LU_HUMAN	P50895 homo sapien
904	79	4.5	222	2	Q8MK98	Q8mk98 macroscelid	977	78.5	4.4	629	2	Q8LA44	Q8la44 arabidopsis
905	79	4.5	226	2	Q86P32	Q86p32 drosophila	978	78.5	4.4	638	2	Q9LFS4	Q9lfs4 arabidopsis
906	79	4.5	244	2	Q927X2	Q927x2 listeria in	979	78.5	4.4	651	2	Q88BU0	Q88bu0 pseudomonas
907	79	4.5	271	2	Q95161	Q95161 gadus morhu	980	78.5	4.4	708	1	KIR2_HUMAN	Q6uw16 homo sapien

981	Q6clh8	717	2	Q6CLH8	Q6clh8	yarrowia li	1054	78	4.4	1229	2	Q6CKW4	Q6ckw4	kluyveromyc
982	Q6FK37	751	1	Q6FK37	Q6fk37	candida glia	1055	78	4.4	1503	2	Q7KTZ4	Q7ktz4	drosophila
983	SAS3 YEAST	831	1	SAS3	P34218	saccharomyc	1056	78	4.4	1924	2	Q7Z8U6	Q7z8u6	aspergillus
984	Q875H9	844	1	Q875H9	Q875h9	candida alb	1057	78	4.4	3722	2	P94873	P94873	lysobacter
985	CD22 HUMAN	847	1	CD22	P20273	homo sapien	1058	77.5	4.4	117	2	Q7ZZ67	Q7zz67	brachydanio
986	Q7ZWM9	888	2	Q7ZWM9	Q7zwm9	xenopus lae	1059	77.5	4.4	128	2	Q86UW2	Q86uw2	homo sapien
987	CDGD HUMAN	927	1	CDGD	Q9Y5G3	homo sapien	1060	77.5	4.4	172	2	Q19627	Q19627	caenorhabdi
988	Q64B03	938	2	Q64B03	Q64bu3	uncultured	1061	77.5	4.4	186	2	Q8MV99	Q8mv99	ixodes scap
989	Q63L89	1018	2	Q63L89	Q63l89	burkholderi	1062	77.5	4.4	202	2	Q7N6H1	Q7n6h1	photothabdi
990	Q62C67	1033	2	Q62C67	Q62c67	burkholderi	1063	77.5	4.4	214	2	Q99VY1	Q99vy1	staphylococ
991	AX01 CHICK	1036	1	AX01	P28685	gallus gall	1064	77.5	4.4	214	2	Q7A1M5	Q7a1m5	staphylococ
992	Q8YSN0	1038	2	Q8YSN0	Q8yen0	anabaena sp	1065	77.5	4.4	214	2	Q7A2T3	Q7a2t3	staphylococ
993	Q69Z28	1143	2	Q69Z28	Q69zz8	mus musculus	1066	77.5	4.4	214	2	Q7A716	Q7a716	staphylococ
994	Q89YU3	1465	2	Q89YU3	Q89yu3	arabidopsis	1067	77.5	4.4	214	2	Q6GBJ6	Q6gbj6	staphylococ
995	Q8SVE1	1468	2	Q8SVE1	Q8svel1	arabidopsis	1068	77.5	4.4	214	2	Q6GJ36	Q6gj36	staphylococ
996	Q7RQM4	1615	2	Q7RQM4	Q7rqm4	plasmodium	1069	77.5	4.4	236	1	YUL1_SCHPO	Y74414	schizosacch
997	Q60612	1788	2	Q60612	Q60612	homo sapien	1070	77.5	4.4	239	1	CD8A_FELCA	P41688	felis silve
998	Q8NEJ1	1815	2	Q8NEJ1	Q8nejl1	homo sapien	1071	77.5	4.4	276	2	Q6P0R7	Q6p0r7	brachydanio
999	Q62P22	1994	2	Q62P22	Q62pp2	mus musculus	1072	77.5	4.4	284	2	Q8NX42	Q8nx42	homo sapien
1000	Q6V4S5	2176	2	Q6V4S5	Q6v4s5	mus musculus	1073	77.5	4.4	294	2	Q8K1Z5	Q8k1z5	mus musculus
1001	Q61VD6	2829	2	Q61VD6	Q61vd6	strongyloce	1074	77.5	4.4	300	2	Q9JHY1	Q9jhy1	rattus norv
1002	Q6UXZ3	194	2	Q6UXZ3	Q6uxz3	homo sapien	1075	77.5	4.4	320	2	Q7Q0P8	Q7q0p8	anopheles g
1003	Q6UXN2	200	2	Q6UXN2	Q6uxn2	homo sapien	1076	77.5	4.4	321	2	Q6UXI4	Q6uxi4	homo sapien
1004	Q8NEJ1	236	2	Q8NEJ1	Q8nejl1	homo sapien	1077	77.5	4.4	324	2	Q940M5	Q940m5	arabidopsis
1005	UPPS_CLOAB	257	1	UPPS	Q97162	clostridium	1078	77.5	4.4	332	2	Q91AZ3	Q91az3	sphoeroides
1006	Q8R1N5	272	2	Q8R1N5	Q8rln5	mus musculus	1079	77.5	4.4	331	2	Q675Z1	Q675z1	oikopleura
1007	Q13984	287	2	Q13984	Q13984	homo sapien	1080	77.5	4.4	333	1	C1B1_CAVPO	Q9qz22	cavia porce
1008	Q6UY47	292	2	Q6UY47	Q6uy47	homo sapien	1081	77.5	4.4	338	2	Q6DHD4	Q6dhd4	brachydanio
1009	Q43754	304	2	Q43754	Q43754	homo sapien	1082	77.5	4.4	345	2	Q9G9W3	Q9g9w3	teleogryllu
1010	Q57596	313	2	Q57596	Q57596	gallus gall	1083	77.5	4.4	345	2	Q9G9W4	Q9g9w4	teleogryllu
1011	PSG5_HUMAN	335	1	PSG5	Q15238	homo sapien	1084	77.5	4.4	351	2	Q9ADX7	Q9adx7	agrobacteri
1012	CEPU_CHICK	353	1	CEPU	Q90773	gallus gall	1085	77.5	4.4	356	2	Q8AXL7	Q8axl7	oncorhynch
1013	Q18353	372	2	Q18353	Q18353	caenorhabdi	1086	77.5	4.4	360	2	Q7VAZ7	Q7vaz7	prochloroco
1014	Q65280	375	2	Q65280	Q65280	african swi	1087	77.5	4.4	368	2	Q6F5F1	Q6f5f1	mus musculus
1015	Q9Y279	399	2	Q9Y279	Q9y279	homo sapien	1088	77.5	4.4	371	2	Q81KQ7	Q81kq7	bacillus an
1016	Q7PSS8	401	2	Q7PSS8	Q7pes8	anopheles g	1089	77.5	4.4	425	2	Q96VU0	Q96vu0	amanita mus
1017	Q35444	402	2	Q35444	Q35444	mus musculus	1090	77.5	4.4	428	2	Q72NX8	Q72nx8	leptospira
1018	Q76PD3	412	2	Q76PD3	Q76pd3	schizosacch	1091	77.5	4.4	428	2	Q8F7J7	Q8f7j7	leptospira
1019	Q9RB12	423	2	Q9RB12	Q9rb12	acinetobact	1092	77.5	4.4	433	2	O55054	O55054	mus musculus
1020	Q7VQM5	452	2	Q7VQM5	Q7vqm5	candidatus	1093	77.5	4.4	448	1	EX7L_STR6	EX7L_STR6	streptococ
1021	Q9VVO5	473	2	Q9VVO5	Q9vvq5	drosophila	1094	77.5	4.4	460	2	Q7YTA8	Q7yta8	bombyx mori
1022	Q74491	490	2	Q74491	Q74491	schizosacch	1095	77.5	4.4	476	2	Q9CU34	Q9cu34	mus musculus
1023	Q9VVKX6	491	2	Q9VVKX6	Q9vkkx6	drosophila	1096	77.5	4.4	490	1	CNAB_MOUSE	CNAB_MOUSE	mus musculus
1024	Q76PD3	604	2	Q76PD3	Q76pd3	schizosacch	1097	77.5	4.4	491	1	SYT9_HUMAN	SYT9_HUMAN	homo sapien
1025	Q6IRH8	606	2	Q6IRH8	Q6irh8	rattus norv	1098	77.5	4.4	510	1	MOQ_WIGBR	Q8dlv2	wiggleswort
1026	Q9BSS7	606	2	Q9BSS7	Q9ess7	mus musculus	1099	77.5	4.4	513	1	SHS1_MOUSE	P97797	m protein-t
1027	Q8YCV9	608	2	Q8YCV9	Q8ycv9	brucella me	1100	77.5	4.4	536	2	Q7UZH7	Q7uzh7	prochloroco
1028	Q8FVG6	608	2	Q8FVG6	Q8fvq6	brucella su	1101	77.5	4.4	539	2	Q9FX24	Q9fx24	arabidopsis
1029	HEWA_RINDK	609	1	HEWA	P12567	rinderpest	1102	77.5	4.4	589	2	Q8RZH3	Q8rzh3	oryza sativ
1030	Q629I1	609	2	Q629I1	Q629i1	rinderpest	1103	77.5	4.4	591	2	Q91IK8	Q91ik8	pseudomonas
1031	Q7RE74	612	2	Q7RE74	Q7re74	plasmodium	1104	77.5	4.4	593	2	Q61NM5	Q61nm5	xenopus lae
1032	Q8X0Z4	634	2	Q8X0Z4	Q8x0z4	cryptococcu	1105	77.5	4.4	603	2	O71ZR6	O71zr6	listeria mo
1033	Q96WKO	634	2	Q96WKO	Q96wx0	cryptococcu	1106	77.5	4.4	611	2	O70W32	O70w32	oncorhynch
1034	Q8R2Y2	648	2	Q8R2Y2	Q8r2y2	mus musculus	1107	77.5	4.4	650	1	LIB1_HUMAN	LIB1_HUMAN	h leukocyte
1035	Q762C5	652	2	Q762C5	Q762c5	mus musculus	1108	77.5	4.4	687	2	Q6CUK2	Q6cuk2	kluyveromyc
1036	Q6YC14	706	2	Q6YC14	Q6yc14	mus musculus	1109	77.5	4.4	717	2	Q8U7P9	Q8u7p9	agrobacteri
1037	Q8BM11	706	2	Q8BM11	Q8bm11	mus musculus	1110	77.5	4.4	725	2	Q6WQQ9	Q6wqq9	bdellovibri
1038	NCA2_HUMAN	761	1	NCA2	P13592	homo sapien	1111	77.5	4.4	735	2	Q9FG24	Q9fg24	arabidopsis
1039	Q48483	836	2	Q48483	Q48483	bacterioph	1112	77.5	4.4	735	1	O85606	O85606	human t-cel
1040	NCA1_HUMAN	848	1	NCA1	P13591	homo sapien	1113	77.5	4.4	739	1	VCAL_HUMAN	VCAL_HUMAN	homo sapien
1041	SMIA_DROME	850	1	SMIA	Q24322	drosophila	1114	77.5	4.4	757	1	DNM1_YEAST	P54861	saccharomyc
1042	Q8Q7H7	865	2	Q8Q7H7	Q8q7h7	human immun	1115	77.5	4.4	785	2	Q6CTN0	Q6ctn0	kluyveromyc
1043	CADB_XENLA	884	1	CADB	P33152	xenopus lae	1116	77.5	4.4	829	2	Q64XJ3	Q64xj3	bacteroides
1044	Q6NTM0	884	2	Q6NTM0	Q6ntm0	xenopus lae	1117	77.5	4.4	912	2	O651Q0	O651q0	oryza sativ
1045	Q13955	905	2	Q13955	Q13955	schizosacch	1118	77.5	4.4	951	2	P91193	P91193	caenorhabdi
1046	Q6LYF8	976	2	Q6LYF8	Q6lyf8	methanococc	1119	77.5	4.4	991	2	Q9S7G6	Q9s7g6	arabidopsis
1047	DSG3_MOUSE	993	1	DSG3	Q95902	mus musculus	1120	77.5	4.4	997	2	O44087	O44087	caenorhabdi
1048	Q7QCM9	1007	2	Q7QCM9	Q7qcm9	anopheles g	1121	77.5	4.4	1014	2	O77813	O77813	oryctolagus
1049	Q93250	1009	2	Q93250	Q93250	xenopus lae	1122	77.5	4.4	1040	2	Q9W675	Q9w675	brachydanio
1050	Q8A4W1	1016	2	Q8A4W1	Q8a4w1	bacteroides	1123	77.5	4.4	1082	2	Q8W0U0	Q8w0u0	sorghum bic
1051	AX01_MOUSE	1040	1	AX01	Q61330	mus musculus	1124	77.5	4.4	1093	2	O6GNA9	O6gna9	xenopus lae
1052	Q75CA6	1071	2	Q75CA6	Q75ca6	ashbya gos	1125	77.5	4.4	1099	2	P90731	P90731	caenorhabdi
1053	Q9DDK1	1147	2	Q9DDK1	Q9ddk1	meleagris g	1126	77.5	4.4	1190	2	Q9DPQ8	Q9dpq8	meleagris h

1127	77.5	4.4	1190	2	Q9E1G3	Q9elg3 meleagrid h	1200	77	4.3	1021	2	Q93033	Q93033 homo sapien
1128	77.5	4.4	1205	2	Q922Y1	Q922y1 rattus norv	1201	77	4.3	1029	2	Q9HWH4	Q9hwh4 pseudomonas
1129	77.5	4.4	1297	2	Q61485	Q61485 oryza sativ	1202	77	4.3	1036	2	Q8SWW3	Q8sww3 drosophila
1130	77.5	4.4	1302	2	Q9S7F1	Q9s7f1 oryza sativ	1203	77	4.3	1037	2	Q8BUH8	Q8buh8 mus musculus
1131	77.5	4.4	1662	2	Q7Q1V4	Q7q1v4 anopheles g	1204	77	4.3	1041	1	EGT2_YEAST	P42835 saccharomyc
1132	77.5	4.4	1894	2	Q64487	Q64487 mus musculus	1205	77	4.3	1044	2	Q861W3	Q861w3 homo sapien
1133	77.5	4.4	1912	1	PTPD_HUMAN	P23468 homo sapien	1206	77	4.3	1051	2	Q80TA3	Q80ta3 mus musculus
1134	77.5	4.4	1950	1	UBR1_YEAST	P19812 saccharomyc	1207	77	4.3	1159	2	Q9YIA6	Q9yia6 cyprinus ca
1135	77.5	4.4	2008	2	Q9VEJ5	Q9vej5 drosophila	1208	77	4.3	1183	2	Q80VV7	Q80vv7 mus musculus
1136	77.5	4.4	2213	2	Q7Z5N4	Q7z5n4 homo sapien	1209	77	4.3	1207	2	Q9V3I5	Q9v3i5 drosophila
1137	77.5	4.4	7105	2	Q7PXW9	Q7pxw9 anopheles g	1210	77	4.3	1230	2	Q8EST9	Q8est9 streptococc
1138	77	4.3	138	1	PSAD_NOSS8	P56596 nostoc sp.	1211	77	4.3	1237	2	Q9NG20	Q9ng20 plasmodium
1139	77	4.3	139	2	Q9R6W5	Q9r6w5 nostoc sp.	1212	77	4.3	1230	2	Q9XZJ6	Q9xzj6 plasmodium
1140	77	4.3	220	2	Q9T4W8	Q9t4w8 cyanophora	1213	77	4.3	1237	2	Q75147	Q75147 homo sapien
1141	77	4.3	223	2	Q8AW68	Q8aw68 brachydanio	1214	77	4.3	1294	2	Q6WLB1	Q6wlb1 epalpus sig
1142	77	4.3	236	2	Q6GMV7	Q6gmv7 homo sapien	1215	77	4.3	1323	2	Q68DY3	Q68dy3 homo sapien
1143	77	4.3	262	2	Q9LA26	Q9la26 shigella dy	1216	77	4.3	1390	2	Q9VN14	Q9vn14 drosophila
1144	77	4.3	262	2	Q83RK3	Q83rk3 shigella fl	1217	77	4.3	1446	2	Q6INI4	Q6ini4 xenopus lae
1145	77	4.3	268	2	Q91BX0	Q91bx0 meleagrid h	1218	77	4.3	1448	1	PK3G_HUMAN	Q75747 homo sapien
1146	77	4.3	278	1	OX2G_MOUSE	O54901 mus musculus	1219	77	4.3	1856	2	Q9USD7	Q9usd7 plautia eta
1147	77	4.3	278	2	Q80VX2	Q80vx2 mus musculus	1220	77	4.3	1897	2	PTPF_HUMAN	P10586 homo sapien
1148	77	4.3	291	2	Q75NT2	Q75nt2 pleurotus o	1221	77	4.3	1898	2	Q86WS0	Q86ws0 homo sapien
1149	77	4.3	296	2	Q64OC0	Q64oc0 xenopus lae	1222	77	4.3	2167	2	Q92EK5	Q92ek5 listeria in
1150	77	4.3	300	2	Q7SVQ7	Q7svq7 xenopus lae	1223	77	4.3	2473	2	Q95LC7	Q95lc7 tachyglossu
1151	77	4.3	311	2	Q8STU5	Q8stu5 encephalito	1224	77	4.3	4834	2	Q95714	Q95714 homo sapien
1152	77	4.3	330	2	Q7NCD8	Q7ncd8 gloebacter	1225	77	4.3	4836	2	O88473	O88473 mus musculus
1153	77	4.3	334	2	Q02870	Q02870 gallus gall	1226	77	4.3	4870	1	RYR3_HUMAN	Q15413 homo sapien
1154	77	4.3	338	1	LAMP_CHICK	Q98919 gallus gall	1227	76.5	4.3	191	1	MOBA_PYRAB	Q9v0d0 pyrococcus
1155	77	4.3	345	2	Q43102	Q43102 populus tri	1228	76.5	4.3	225	2	Q6PAF5	Q6paf5 xenopus lae
1156	77	4.3	350	2	Q02869	Q02869 gallus gall	1229	76.5	4.3	235	2	Q75296	Q75296 homo sapien
1157	77	4.3	398	2	Q9LM60	Q9lm60 arabidopsis	1230	76.5	4.3	236	2	Q701Y6	Q701y6 uncultured
1158	77	4.3	409	2	Q86SV7	Q86sv7 homo sapien	1231	76.5	4.3	236	2	Q6L0J5	Q6l0j5 picophilus
1159	77	4.3	413	2	Q7QHG4	Q7qhg4 drosophila	1232	76.5	4.3	236	2	Q15461	Q15461 homo sapien
1160	77	4.3	428	2	Q7QVAR6	Q7qvar6 anopheles g	1233	76.5	4.3	238	2	Q9XTE8	Q9xte8 caenorhabdi
1161	77	4.3	431	2	Q7W3V9	Q7w3v9 prochloroco	1234	76.5	4.3	251	2	P73200	P73200 synchocyst
1162	77	4.3	433	2	Q9NIN3	Q9nin3 armadillidi	1235	76.5	4.3	276	2	Q6INX3	Q6inx3 xenopus lae
1163	77	4.3	439	2	Q05919	Q05919 saccharomyc	1236	76.5	4.3	281	2	Q6UC84	Q6uc84 gallus gall
1164	77	4.3	439	2	Q6BIJ7	Q6bij7 saccharomyc	1237	76.5	4.3	283	2	Q8K4V9	Q8k4v9 mus musculus
1165	77	4.3	446	2	Q13006	Q13006 ictalurisc p	1238	76.5	4.3	296	2	Q9KQJ7	Q9kqj7 vibrio chol
1166	77	4.3	447	2	Q7YRY6	Q7yry6 gorilla gor	1239	76.5	4.3	298	2	Q8C5K9	Q8c5k9 mus musculus
1167	77	4.3	456	2	Q6GAH0	Q6gah0 staphylococ	1240	76.5	4.3	318	2	Q8ZKN7	Q8zkn7 pyrobaculum
1168	77	4.3	462	2	Q8BCU0	Q8bcu0 human cytom	1241	76.5	4.3	320	2	O86869	O86869 streptomyc
1169	77	4.3	479	2	Q7TAK4	Q7tak4 mus musculus	1242	76.5	4.3	323	2	Q8KSD9	Q8ksd9 mus musculus
1170	77	4.3	480	2	Q13007	Q13007 ictalurisc p	1243	76.5	4.3	339	2	Q9IAY8	Q9iay8 spherooides
1171	77	4.3	491	1	KCS3_RAT	Q88759 rattus norv	1244	76.5	4.3	370	2	Q6MZQ3	Q6mzq3 homo sapien
1172	77	4.3	497	2	Q9BXN7	Q9bxn7 homo sapien	1245	76.5	4.3	371	2	Q7ZU88	Q7zu88 brachydanio
1173	77	4.3	502	1	SKS1_YEAST	Q12505 saccharomyc	1246	76.5	4.3	378	2	Q83DQ8	Q83dq8 coxiella bu
1174	77	4.3	523	1	CP78_SOYEN	O48927 glycine max	1247	76.5	4.3	390	2	Q9LWR2	Q9lwr2 arabidopsis
1175	77	4.3	529	2	Q7TQM3	Q7tqm3 rattus norv	1248	76.5	4.3	402	2	Q15227	Q15227 homo sapien
1176	77	4.3	532	2	Q64HW6	Q64hw6 oncorhynch	1249	76.5	4.3	413	2	Q699P0	Q699p0 antheraea p
1177	77	4.3	543	2	Q8C7W8	Q8c7w8 mus musculus	1250	76.5	4.3	423	2	Q8Y9J1	Q8y9j1 listeria mo
1178	77	4.3	570	2	Q8H060	Q8h060 oryza sativ	1251	76.5	4.3	426	1	PSG9_HUMAN	Q00887 homo sapien
1179	77	4.3	577	2	Q80V42	Q80v42 mus musculus	1252	76.5	4.3	432	2	Q6LEU7	Q6leu7 homo sapien
1180	77	4.3	609	2	Q6MMG1	Q6mmg1 bdellovibri	1253	76.5	4.3	432	2	O88463	O88463 mus musculus
1181	77	4.3	632	2	Q6BL77	Q6bl77 debaryomyc	1254	76.5	4.3	452	1	Q7NDI5	Q7ndi5 gloebacter
1182	77	4.3	706	2	Q8ZXU6	Q8zxu6 pyrobaculum	1255	76.5	4.3	458	1	CD4_MACNE	Q08340 macaca neme
1183	77	4.3	709	2	Q9FHY2	Q9fhy2 arabidopsis	1256	76.5	4.3	463	2	Q8BCT9	Q8bct9 human cytom
1184	77	4.3	712	2	Q65LR5	Q65lr5 bacillus li	1257	76.5	4.3	473	2	Q6DHN9	Q6dhn9 brachydanio
1185	77	4.3	723	2	Q69VK3	Q69vk3 oryza sativ	1258	76.5	4.3	485	2	Q9HLC1	Q9hlc1 thermoplasm
1186	77	4.3	736	2	Q6JU60	Q6ju60 armadillidi	1259	76.5	4.3	497	1	UBID_ECOLI	P2615 escherichia
1187	77	4.3	750	2	Q9ZPF8	Q9zpf8 burkholderi	1260	76.5	4.3	501	2	Q6Q147	Q6q147 bos taurus
1188	77	4.3	757	2	Q62G71	Q62g71 burkholderi	1261	76.5	4.3	523	2	Q8ZKH7	Q8zkh7 mus musculus
1189	77	4.3	757	2	Q63230	Q63230 burkholderi	1262	76.5	4.3	582	2	Q9ZLC5	Q9zlc5 helicobacte
1190	77	4.3	759	2	Q7R9A5	Q7r9a5 plasmodium	1263	76.5	4.3	608	2	Q7S8A4	Q7s8a4 neurospora
1191	77	4.3	769	2	Q8W0S7	Q8w0s7 sorghum bic	1264	76.5	4.3	610	2	Q9N505	Q9n505 caenorhabdi
1192	77	4.3	796	2	Q8X212	Q8x212 talaromyces	1265	76.5	4.3	632	2	Q8UW33	Q8uw33 gallus gall
1193	77	4.3	873	1	LDVR_RABIT	P35953 oryctolagus	1266	76.5	4.3	709	2	Q7RCD4	Q7rcd4 plasmodium
1194	77	4.3	881	2	Q8ISG6	Q8isg6 stylonychia	1267	76.5	4.3	727	2	O45675	O45675 caenorhabdi
1195	77	4.3	894	1	MTP_MOUSE	O08601 mus musculus	1268	76.5	4.3	748	2	Q6R7E1	Q6r7e1 oestrid her
1196	77	4.3	894	2	Q91X33	Q91x33 mus musculus	1269	76.5	4.3	768	2	Q88G76	Q88g76 pseudomonas
1197	77	4.3	911	2	Q9W2S8	Q9w2s8 drosophila	1270	76.5	4.3	788	2	Q83035	Q83035 la france d
1198	77	4.3	977	2	Q6NXV8	Q6nxv8 mus musculus	1271	76.5	4.3	833	2	Q6FKV7	Q6fkv7 candida gla
1199	77	4.3	988	2	Q6SLB1	Q6slb1 gibberella	1272	76.5	4.3	839	1	DRL4_ARATH	Q9sx38 arabidopsis

1273	Q9QWH1	2	850	4.3	76.5	Q9qwh1 mus musculus	1346	76	4.3	507	2	Q9ZC47	Q9zc47 yersinia pe
1274	Q39143	2	876	4.3	76	Q39143 arabisopsis	1347	76	4.3	508	2	Q8ZF21	Q8zf21 yersinia pe
1275	Q9SZV2	2	934	4.3	76	Q9szv2 arabisopsis	1348	76	4.3	509	2	Q86B45	Q86b45 yersinia ps
1276	Q8BRRO	2	923	4.3	76	Q8brro mus musculus	1349	76	4.3	509	2	Q8D0C9	Q8d0c9 yersinia pe
1277	Q7XDJ7	2	982	4.3	76	Q7xdj7 oryza sativ	1350	76	4.3	524	1	BUTY_MOUSE	Q82556 mus musculus
1278	Q9FWMO	2	982	4.3	76	Q9fwm0 oryza sativ	1351	76	4.3	550	2	Q97UB3	Q97ub3 sulfolobus
1279	Q7JNZ0	2	1004	4.3	76	Q7jnz0 caenorhabdi	1352	76	4.3	555	2	Q8NEP2	Q8nep2 corynebacte
1280	Q9BL11	2	1019	4.3	76	Q9bl11 caenorhabdi	1353	76	4.3	568	2	Q8JKQ6	Q8jkg6 heliothis z
1281	Q6NXV7	2	1020	4.3	76	Q6nxv7 mus musculus	1354	76	4.3	599	2	Q82M54	Q82m54 streptomyce
1282	Q9ULI7	2	1023	4.3	76	Q9uli7 homo sapien	1355	76	4.3	609	2	Q86496	Q86496 rinderpest
1283	Q8LMF3	2	1042	4.3	76	Q8lmf3 oryza sativ	1356	76	4.3	631	2	Q6D8S1	Q6d8s1 xenopus lae
1284	Q17644	2	1043	4.3	76	Q17644 caenorhabdi	1357	76	4.3	659	2	Q84785	Q84786 uncultured
1285	SEFI_KLJULA	1	1087	4.3	76	P87164 kluyveromyc	1358	76	4.3	709	2	Q9YIY7	Q9yiy7 ephydatia f
1286	PGDS_HUMAN	1	1089	4.3	76	P16234 homo sapien	1359	76	4.3	761	2	Q9UVJ1	Q9uvj1 candida alb
1287	TCF8_HUMAN	1	1124	4.3	76	P37275 homo sapien	1360	76	4.3	780	2	Q6BPD5	Q6bpd5 debaryomyce
1288	Q90WM2	2	1152	4.3	76	Q90wm2 xenopus lae	1361	76	4.3	828	2	Q6P995	Q6p995 homo sapien
1289	Q13088	2	1154	4.3	76	Q13088 homo sapien	1362	76	4.3	836	2	Q8W5F4	Q8w5f4 oryza sativ
1290	N133_HUMAN	1	1156	4.3	76	Q8wum0 homo sapien	1363	76	4.3	836	2	Q7XFQ8	Q7xfq8 oryza sativ
1291	Q90Z04	2	1249	4.3	76	Q90z04 xenopus lae	1364	76	4.3	841	2	O22289	O22289 arabisopsis
1292	Q96DN3	2	1252	4.3	76	Q96dn3 homo sapien	1365	76	4.3	846	2	O57577	O57577 cynops pyrr
1293	Q13264	2	1264	4.3	76	Q13264 homo sapien	1366	76	4.3	847	2	Q73GE5	Q73ge5 wlbachia p
1294	Q14631	2	1314	4.3	76	Q14631 oryza sativ	1367	76	4.3	907	2	Q6FRX9	Q6frx9 candida gla
1295	Q7XTI8	2	1328	4.3	76	Q7xti8 oryza sativ	1368	76	4.3	937	2	Q8GYR5	Q8gyr5 caenorhabdi
1296	HUS2_SCHPO	1	1354	4.3	76	Q09811 schizosacch	1369	76	4.3	964	2	Q18382	Q18382 caenorhabdi
1297	Q9W6B2	2	1354	4.3	76	Q9w6b2 xenopus lae	1370	76	4.3	977	1	KFMS_MOUSE	KFMS_MOUSE
1298	Q1461	2	1461	4.3	76	O05819 mycobacteri	1371	76	4.3	978	1	KFMS_RAT	KFMS_RAT
1299	Q7TYQ8	2	1461	4.3	76	Q7tyq8 mycobacteri	1372	76	4.3	1018	2	Q28106	Q28106 bos taurus
1300	Q7BX13	2	1479	4.3	76	Q7bx13 neurospora	1373	76	4.3	1019	2	Q6P915	Q6p915 xenopus lae
1301	Q17344	2	1786	4.3	76	Q17344 caenorhabdi	1374	76	4.3	1028	2	P97528	P97528 rattus norv
1302	Q87310	2	1792	4.3	76	Q87310 neurospora	1375	76	4.3	1093	2	Q9LFE6	Q9lfe6 arabisopsis
1303	HKR1_YEAST	1	1802	4.3	76	P14809 saccharomyc	1376	76	4.3	1100	2	O57576	O57576 cynops pyrr
1304	Q17487	2	1809	4.3	76	Q17487 caenorhabdi	1377	76	4.3	1165	2	Q7TP57	Q7tp57 rattus norv
1305	Q17488	2	1815	4.3	76	Q17488 caenorhabdi	1378	76	4.3	1196	2	Q65Z10	Q65z10 caenorhabdi
1306	Q8MQG0	2	1841	4.3	76	Q8mqg0 caenorhabdi	1379	76	4.3	1227	2	Q9BIA2	Q9bia2 caenorhabdi
1307	Q17486	2	1867	4.3	76	Q17486 caenorhabdi	1380	76	4.3	1322	2	Q8IHZ8	Q8ihz8 plasmodium
1308	Q17489	2	2039	4.3	76	Q17489 caenorhabdi	1381	76	4.3	1331	2	Q7Q623	Q7q623 anopheles g
1309	Q7BQ70	2	2562	4.3	76	Q7bq70 bacillus ce	1382	76	4.3	1540	2	Q7RMI6	Q7rm16 plasmodium
1310	Q86W11	2	4243	4.3	76	Q86w11 homo sapien	1383	76	4.3	1654	2	Q6BG97	Q6bg97 paramedum
1311	Q7YT99	2	4736	4.3	76	Q7yt99 mytilus gal	1384	76	4.3	1703	2	Q7R355	Q7r355 giardia lam
1312	Q17343	2	6994	4.3	76	Q17343 caenorhabdi	1385	76	4.3	1933	2	Q6V3A4	Q6v3a4 mus musculus
1313	Q17490	2	6994	4.3	76	Q17490 caenorhabdi	1386	76	4.3	2029	1	LAR_DROME	LAR_DROME
1314	PSAD_FREDI	1	138	4.3	76	P23808 fremyella d	1387	76	4.3	2029	2	Q9VIS8	Q9vis8 drosophila
1315	Q8Y8V8	2	144	4.3	76	Q8y8v8 listeria mo	1388	76	4.3	2104	2	Q8XM24	Q8xm24 clostridium
1316	Q63P25	2	218	4.3	76	Q63p25 burkholderi	1389	76	4.3	2159	2	Q6PAL2	Q6pal2 mus musculus
1317	Q45629	2	239	4.3	76	Q45629 caenorhabdi	1390	76	4.3	2747	2	Q91800	Q91800 aeromonas s
1318	Q9FUB1	2	254	4.3	76	Q9fub1 oryza sativ	1391	76	4.3	3027	2	Q7MB03	Q7mb03 photorhabdu
1319	YCIJ_ECOLI	2	262	4.3	76	P51983 escherichia	1392	76	4.3	3347	2	Q8IEA1	Q8iea1 plasmodium
1320	Q69ZQ3	2	268	4.3	76	Q69zq3 mus musculus	1393	76	4.3	3941	2	Q6RKJ7	Q6rkj7 botrytis ci
1321	Q8BTP3	2	270	4.3	76	Q8btp3 mus musculus	1394	76	4.3	4071	2	Q6K0Z1	Q6kdz1 gallus gall
1322	Q97KM4	2	286	4.3	76	Q97km4 clostridium	1395	76	4.3	4249	2	Q80ZA4	Q80za4 mus musculus
1323	Q94398	2	305	4.3	76	P94398 bacillus su	1396	75.5	4.3	193	2	Q7QGT6	Q7qgt6 anopheles g
1324	Q9DDF0	2	311	4.3	76	Q9ddf0 geochelone	1397	75.5	4.3	246	1	MOG_BOVIN	P55803 bos taurus
1325	DDL_ENTGA	1	316	4.3	76	Q47823 enterococcu	1398	75.5	4.3	262	2	Q9FT14	Q9ft14 brassica na
1326	Q69ZQ3	2	316	4.3	76	Q47823 enterococcu	1399	75.5	4.3	272	2	Q861N0	Q861n0 equus cabal
1327	AMAL_DROME	1	333	4.3	76	P15364 drosophila	1400	75.5	4.3	272	2	Q861N1	Q861n1 equus cabal
1328	Q8UV73	2	336	4.3	76	Q8uv73 brachydanio	1401	75.5	4.3	280	2	Q73716	Q73716 grus ameri
1329	Q7KX2	2	341	4.3	76	Q7kx2 drosophila	1402	75.5	4.3	283	2	Q70LN8	Q70ln8 pasteurella
1330	Q8JG5	2	351	4.3	76	Q8jg5 enterococcu	1403	75.5	4.3	298	2	Q8CE95	Q8ce95 mus musculus
1331	Q9W6V2	2	352	4.3	76	Q9w6v2 gallus gall	1404	75.5	4.3	308	2	Q8VZP4	Q8vzp4 arabisopsis
1332	Q8GW61	2	354	4.3	76	Q8gw61 homo sapien	1405	75.5	4.3	321	1	TCB_FLV	P13364 feline leux
1333	Q8BS97	2	368	4.3	76	Q8bs97 mus musculus	1406	75.5	4.3	330	2	Q7TRZ7	Q7trz7 mus musculus
1334	Q93GE2	2	369	4.3	76	Q93ge2 desulfotona	1407	75.5	4.3	344	2	Q8BF61	Q8bf61 gallus gall
1335	Q86JM7	2	378	4.3	76	Q86jm7 dictyosteli	1408	75.5	4.3	344	2	Q9DF61	Q9df61 gallus gall
1336	Q60667	2	390	4.3	76	Q60667 homo sapien	1409	75.5	4.3	352	2	Q84DD2	Q84dd2 uncultured
1337	Q9LG22	2	414	4.3	76	Q9lg22 arabisopsis	1410	75.5	4.3	353	2	Q8GCX2	Q8gcx2 enterococcu
1338	PGCB_FELCA	1	417	4.3	76	P41725 felis silve	1411	75.5	4.3	367	2	Q9GJE4	Q9gje4 fugu rubrip
1339	Q762C7	2	426	4.3	76	Q762c7 homo sapien	1412	75.5	4.3	370	2	Q7TSN7	Q7tsn7 mus musculus
1340	Q8MK39	2	440	4.3	76	Q8mk39 macaca mula	1413	75.5	4.3	373	2	Q821Z1	Q821z1 chlamydropi
1341	Q8XQX4	2	459	4.3	76	Q8qx4 ralstonia s	1414	75.5	4.3	382	2	Q8XKW8	Q8xkw8 clostridium
1342	Q7Z4G4	2	463	4.3	76	Q7z4g4 homo sapien	1415	75.5	4.3	392	2	Q8CUH4	Q8cuh4 kluyveromyc
1343	DPD2_YEAST	1	487	4.3	76	P46957 saccharomyc	1416	75.5	4.3	393	2	Q95727	Q95727 homo sapien
1344	Q65ZL2	2	487	4.3	76	Q65zl2 mus sp. fv/	1417	75.5	4.3	419	2	Q24548	Q24548 drosophila
1345	Q81WS7	2	490	4.3	76	Q81ws7 homo sapien	1418	75.5	4.3	421	1	MFR1_SCHPO	Q94423 schizosacch



DR Genew; HGNC:21394; SLAMF7.  
 DR GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR007110; IG-like.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Receptor.  
 SQ SEQUENCE 335 AA; 37421 MW; D09ABBCFF74B8D4 CRC64;

Query Match 100.0%; Score 1772; DB 2; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-138;  
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPTCLTLIYLWLTGSAASGPVKELVSGVAVTFPLKSKVKQVDSIWTNTTTL 60  
 DB 1 MAGSPTCLTLIYLWLTGSAASGPVKELVSGVAVTFPLKSKVKQVDSIWTNTTTL 60

QY 61 VTIOPEGGTTIIVTQNRNRERVDPPDGGYSLKSLKKNDSGIYYVIGIYSSSLQOQSTQY 120  
 DB 61 VTIOPEGGTTIIVTQNRNRERVDPPDGGYSLKSLKKNDSGIYYVIGIYSSSLQOQSTQY 120

QY 121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGQAANESHGSL 180  
 DB 121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGQAANESHGSL 180

QY 181 PISRWGSDMTFICVARNPVSRNFSPPILARKLCEGAADDPDSSNVLCLLLVPLLSSL 240  
 DB 181 PISRWGSDMTFICVARNPVSRNFSPPILARKLCEGAADDPDSSNVLCLLLVPLLSSL 240

QY 241 FVLGLFWLFLKREOEYIEBKRVDI CRETPNICPHSGENTYDTIPTHTNRILKEDPA 300  
 DB 241 FVLGLFWLFLKREOEYIEBKRVDI CRETPNICPHSGENTYDTIPTHTNRILKEDPA 300

QY 301 NTVYSTVEIPKKNMHPHSLLTMPDTPRLPAYENVI 335  
 DB 301 NTVYSTVEIPKKNMHPHSLLTMPDTPRLPAYENVI 335

RESULT 2  
 QYNY08 ID QYNY08 PRELIMINARY; PRT; 335 AA.  
 AC QYNY08;  
 DT 01-OCT-2000 (TremBLrel. 15, Created)  
 DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)  
 DE 19A protein.  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Murphy J.J., Norton J.D.;  
 RT "Cell type specific early response gene expression during plasmacytoid differentiation of human B lymphocytic leukaemia cells.";  
 RL Biochim. Biophys. Acta 1049:262-271(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21661458; PubMed-11802771; DOI=10.1042/0264-6021.3610431;  
 RA Murphy J.J., Hobby P., Villarino-Varela J., Bishop B., Iordanidou P., Sutton B.J., Norton J.D.;  
 RT "A novel immunoglobulin superfamily receptor (19A) related to CD2 is expressed on activated lymphocytes and promotes homotypic B-cell adhesion.";  
 RL Biochem. J. 361:431-436(2002).  
 DR EMBL; AJ276429; CAB81950.2; --  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR SMART; SM00409; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 SQ SEQUENCE 335 AA; 37403 MW; BB758B505CA4DD5 CRC64;

Query Match 99.8%; Score 1769; DB 2; Length 335;  
 Best Local Similarity 99.7%; Pred. No. 1.1e-138;

Matches 334; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPTCLTLIYLWLTGSAASGPVKELVSGVAVTFPLKSKVKQVDSIWTNTTTL 60  
 DB 1 MAGSPTCLTLIYLWLTGSAASGPVKELVSGVAVTFPLKSKVKQVDSIWTNTTTL 60

QY 61 VTIOPEGGTTIIVTQNRNRERVDPPDGGYSLKSLKKNDSGIYYVIGIYSSSLQOQSTQY 120  
 DB 61 VTIOPEGGTTIIVTQNRNRERVDPPDGGYSLKSLKKNDSGIYYVIGIYSSSLQOQSTQY 120

QY 121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGQAANESHGSL 180  
 DB 121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGQAANESHGSL 180

QY 181 PISRWGSDMTFICVARNPVSRNFSPPILARKLCEGAADDPDSSNVLCLLLVPLLSSL 240  
 DB 181 PISRWGSDMTFICVARNPVSRNFSPPILARKLCEGAADDPDSSNVLCLLLVPLLSSL 240

QY 241 FVLGLFWLFLKREOEYIEBKRVDI CRETPNICPHSGENTYDTIPTHTNRILKEDPA 300  
 DB 241 FVLGLFWLFLKREOEYIEBKRVDI CRETPNICPHSGENTYDTIPTHTNRILKEDPA 300

QY 301 NTVYSTVEIPKKNMHPHSLLTMPDTPRLPAYENVI 335  
 DB 301 NTVYSTVEIPKKNMHPHSLLTMPDTPRLPAYENVI 335

RESULT 3  
 QYNY23 ID QYNY23 PRELIMINARY; PRT; 328 AA.  
 AC QYNY23;  
 DT 01-OCT-2000 (TremBLrel. 15, Created)  
 DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)  
 DE 19A24 protein.  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peripheral blood;  
 RA Murphy J.J., Norton J.D., Hobby P., Sutton B.J.;  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ271869; CAB76561.1; --  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR SMART; SM00409; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 SQ SEQUENCE 328 AA; 36490 MW; E68A7243964380DB CRC64;

Query Match 78.6%; Score 1392.5; DB 2; Length 328;  
 Best Local Similarity 86.4%; Pred. No. 3.3e-107;  
 Matches 273; Conservative 3; Mismatches 5; Indels 35; Gaps 3;

QY 1 MAGSPTCLTLIYLWLTGSAASGPVKELVSGVAVTFPLKSKVKQVDSIWTNTTTL 60  
 DB 1 MAGSPTCLTLIYLWLTGSAASGPVKELVSGVAVTFPLKSKVKQVDSIWTNTTTL 60

QY 61 VTIOPEGGTTIIVTQNRNRERVDPPDGGYSLKSLKKNDSGIYYVIGIYSSSLQOQSTQY 120  
 DB 61 VTIOPEGGTTIIVTQNRNRERVDPPDGGYSLKSLKKNDSGIYYVIGIYSSSLQOQSTQY 120

QY 121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGQAANESHGSL 180  
 DB 121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGQAANESHGSL 180

QY 181 PISRWGSDMTFICVARNPVSRNFSPPILARKLCEGAADDPDSSNVLCLLLVPLLSSL 240  
 DB 181 PISRWGSDMTFICVARNPVSRNFSPPILARKLCEGAADDPDSSNVLCLLLVPLLSSL 240

QY 241 FVLGLFWLFLKREOEYIEBKRVDI CRETPNICPHSGENTYDTIPTHTNRILKEDPA 300

```
Db 241 FVLGLFLWFLKRRQEE-----NNP-----KGRSSKYG----- 268
QY 301 NTVYSTVEIPKQWENP 316
Db 269 ---YSTVEIPKQWENP 281

RESULT 4
Q8NGY8 PRELIMINARY; PRT; 296 AA.
AC Q8NGY8;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-WAR-2004 (TremBLrel. 26, Last annotation update)
DE SLAMF7 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RESULT 5
Q8ND32 PRELIMINARY; PRT; 228 AA.
AC Q8ND32;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp667F126;
GN Name=DKFZp667F126;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RG The German cDNA Consortium;
RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834424; CAD39085.1; -
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 228 AA; 25831 MW; 2B01DB70E7BBFC14 CRC64;

Query Match 65.5%; Score 1160.5; DB 2; Length 228;
Best Local Similarity 68.1%; Pred. No. 3.9e-88;
Matches 228; Conservative 0; Mismatches 0; Indels 107; Gaps 1;

QY 1 MAGSPCTCLTIYILWOLGSAAGPVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 60
Db 1 MAGSPCTCLTIYILWOLGSAAGPVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 18
QY 61 VTIOEGGTIIYQNRNRVDFPDGGYSLKSLKKNDSGIYVGYSSSIQQPSTQBY 120
Db 19 ----- 18
QY 121 VLHVYHLSPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180
Db 19 -----EHLSPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 73
QY 181 PISRWGESDMTFFICVARNPVSRNPFSSPILARKLCEGAADDPSSMVLCLLLVPLLSL 240
Db 74 PISRWGESDMTFFICVARNPVSRNPFSSPILARKLCEGAADDPSSMVLCLLLVPLLSL 133
QY 241 FVLGLFLWFLKRRQEEYIEKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPA 300
Db 134 FVLGLFLWFLKRRQEEYIEKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPA 193
QY 301 NTVYSTVEIPKQWENPHSLTMTPTPRLPAYENVI 335
Db 194 NTVYSTVEIPKQWENPHSLTMTPTPRLPAYENVI 228

RESULT 6
Q8BHK6 PRELIMINARY; PRT; 333 AA.
AC Q8BHK6;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:432702H22 product:SIMILAR TO 19A24 PROTEIN homolog
DE (Mus musculus adult male testis cDNA, RIKEN full-length enriched
```

```
Db 241 FVLGLFLWFLKRRQEE-----NNP-----KGRSSKYG----- 268
QY 301 NTVYSTVEIPKQWENP 316
Db 269 ---YSTVEIPKQWENP 281

RESULT 4
Q8NGY8 PRELIMINARY; PRT; 296 AA.
AC Q8NGY8;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-WAR-2004 (TremBLrel. 26, Last annotation update)
DE SLAMF7 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RESULT 5
Q8ND32 PRELIMINARY; PRT; 228 AA.
AC Q8ND32;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp667F126;
GN Name=DKFZp667F126;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RG The German cDNA Consortium;
RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834424; CAD39085.1; -
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 228 AA; 25831 MW; 2B01DB70E7BBFC14 CRC64;

Query Match 65.5%; Score 1160.5; DB 2; Length 228;
Best Local Similarity 68.1%; Pred. No. 3.9e-88;
Matches 228; Conservative 0; Mismatches 0; Indels 107; Gaps 1;

QY 1 MAGSPCTCLTIYILWOLGSAAGPVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 60
Db 1 MAGSPCTCLTIYILWOLGSAAGPVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 18
QY 61 VTIOEGGTIIYQNRNRVDFPDGGYSLKSLKKNDSGIYVGYSSSIQQPSTQBY 120
Db 19 ----- 18
QY 121 VLHVYHLSPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180
Db 19 -----EHLSPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 73
QY 181 PISRWGESDMTFFICVARNPVSRNPFSSPILARKLCEGAADDPSSMVLCLLLVPLLSL 240
Db 74 PISRWGESDMTFFICVARNPVSRNPFSSPILARKLCEGAADDPSSMVLCLLLVPLLSL 133
QY 241 FVLGLFLWFLKRRQEEYIEKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPA 300
Db 134 FVLGLFLWFLKRRQEEYIEKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPA 193
QY 301 NTVYSTVEIPKQWENPHSLTMTPTPRLPAYENVI 335
Db 194 NTVYSTVEIPKQWENPHSLTMTPTPRLPAYENVI 228

RESULT 6
Q8BHK6 PRELIMINARY; PRT; 333 AA.
AC Q8BHK6;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:432702H22 product:SIMILAR TO 19A24 PROTEIN homolog
DE (Mus musculus adult male testis cDNA, RIKEN full-length enriched
```





Db 61 AMVKDGG---VTSQSSNKERIVPPDGLYSNKLSQLKNDGSGAYRABIYSTSSQASLIQBY 117  
Qy 121 VLHVYHLSPKPKVTMGLOSKNGTCTVNTLTCMEHGEEDVIYTWKALGOAANESHGSL 180  
Db 118 VLHVYHLSPKPKVTIDRQSKNGTCTVNTLTCSDQDGENVTYSWKAAGQDQFHDGATL 177  
Qy 181 PISWRMGESDMTFCVARNPVSNSFSPILARKLCEGAADDPDSSWVLLCLLVLPLLSL 240  
Db 178 STAWRSGEKDQALTCWARPVSNSFSTVPFPQKLCEDATDLTSLRGILYLILCFSVAVL 237  
Qy 241 FVLGLF-----WFLKREOEYIEKKRVDICRETNICPHSGENTYDTIPTHTNLTILK 296  
Db 238 FAVLLTIFHTWIKKKGCE---EDKKRVDHGEQMDLCPHLEENADYDTIPTYKRRPE 294  
Qy 297 EDAPNTVYSTVEIPKKNEN---PHSLTWP 323  
Db 295 EDAPNTVYSTVQIPKVRSCPAEHLTCOP 324

RESULT 8  
Q8BTL2 PRELIMINARY; PRT; 335 AA.  
AC Q8BTL2; 01-MAR-2003 (T-EMBLrel. 23, Created)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
DE Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F730045P10 product:SIMILAR TO 19A24  
DE PROTEIN homolog.  
GN Names=Slamf7;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1] SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning."  
RN Meth. Enzymol. 303:19-44(1999).  
[2] SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RX MEDLINE=21085650; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RN Nature 409:685-690(2001).  
[3] SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."  
RN Genome Res. 10:1617-1630(2000).  
[5] SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Kitsumai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."  
RN Genome Res. 10:1757-1771(2000).  
[6] SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK089525; BAC40914.1; -;  
DR MGD; MGI:1922595; Slamf7.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR InterPro; IPR007110; IG-Like.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
SQ SEQUENCE 335 AA; 37521 MW; 99E8802E55A98A03 CRC64;  
Query Match 43.7%; Score 773.5; DB 2; Length 335;  
Best Local Similarity 48.8%; Pred. No. 8.3e-56;  
Matches 161; Conservative 56; Mismatches 100; Indels 13; Gaps 5;  
Qy 1 MAGSTCLTLLIILWOLTSASAGPVELVSGVGAATPPLSKVKQVDSIYVTFVTPPL 60  
Db 1 MARFSTYIIFTSVLCQLTVTAASGLTKKVGALDGSVTFNLNTEIKVYVYVVFTEFFL 60  
Qy 61 VTIQEGGTIIYTONRERVDPPGGYSKLKSKLKNDSGIYVYGVSSSQPSTOEY 120  
Db 61 AMVKDGG---VTSQSSNKERIVPPDGLYSNKLSQLKNDGSGAYRABIYSTSSQASLIQBY 117  
Qy 121 VLHVYHLSPKPKVTMGLOSKNGTCTVNTLTCMEHGEEDVIYTWKALGOAANESHGSL 180  
Db 118 VLHVYHLSPKPKVTIDRQSKNGTCTVNTLTCSDQDGENVTYSWKAAGQDQFHDGATL 177  
Qy 181 PISWRMGESDMTFCVARNPVSNSFSPILARKLCEGAADDPDSSWVLLCLLVLPLLSL 240  
Db 178 STAWRSGEKDQALTCWARPVSNSFSTVPFPQKLCEDATDLTSLRGILYLILCFSVAVL 237  
Qy 241 F--VLGLF--LWFLKREOEYIEKKRVDICRETNICPHSGENTYDTIPTHTNLTILK 296  
Db 238 FAVLLTIFHTWIKKKGCE---EDKKRVDHGEQMDLCPHLEENADYDTIPTYKRRPE 294  
Qy 297 EDAPNTVYSTVEIPKKNEN---PHSLTWP 323  
Db 295 EDAPNTVYSTVQIPKVRSCPAEHLTCOP 324

RESULT 9  
Q8CJ65 PRELIMINARY; PRT; 335 AA.  
AC Q8CJ65; 01-MAR-2003 (T-EMBLrel. 23, Created)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
DE Leukocyte cell-surface antigen.  
GN Name=Slamf7;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1] SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;

```

RX MEDLINE=22226696; PubMed=12242590; DOI=10.1007/s00251-002-0483-3;
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
RA Bosch J., Terhorst C., Engel P.;
RT "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of
RT leukocyte cell-surface receptors.";
RL Immunogenetics 54:394-402(2002).
DR EMBL; AF467909; AAN63158.1; -.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 335 AA; 37493 MW; C210E9CEADC8F3EB CRC64;

Query Match 43.4%; Score 769.5; DB 2; Length 335;
Best Local Similarity 48.5%; Pred. No. 1.8e-55;
Matches 160; Conservative 56; Mismatches 101; Indels 13; Gaps 5;

QY 1 MAGSPTCLTLIIVLWLTGSAAGSPVKELVSGVGAFTPLKSKVKQVDSIVWTNTTPL 60
Db 1 MARFSTYIIFTSVLQCLITVTAASGTLKKVAGALDGSVFTLNLTEIKVDYVVTNTTFFL 60
QY 61 VTIOPEGGTIIIVTONRNRERVDPPGGYSLKSLKKNDSGIYVYGVYSSSLQOYSTOY 120
Db 61 AMVKKDG---VTSQSSNKERIVFPDGLYSMLKSLQKNDGSGAYRAEIVYSTSSQASLIQY 117
QY 121 VLHVYHLSPKPVTVMLGLOSNGKTCVNLTCMEHGEEDVIYTWKALGOAANESHGSL 180
Db 121 ALHVYKLSRPKVTIDRQSNKGTCTVNLTCSDQDGENVTYSKAVGQGNQFHDGATL 177
QY 181 PISRWGSDMTFICVARNPVSRNPFSSPILARKLCEGAADDPDSSMVLCLLLVPLLSL 240
Db 178 SIARSGEKDALTCWARPVNSFSTPVPQKLCEDAATDLTSLRGILYILCFSAVLIL 237
QY 241 F--VLGLF---LWFLKRQEEYIEKKRVDICRETPNICPHSGENTYDTPHTNRTILK 296
Db 238 FAVLLTIPTHTTWIKKGRKP---EKKRVDHREQMPDLCFHLNEADYDTPYTKRRPE 294
QY 297 EDPANTVSTVTEIPKKMEN---PHSLLTMP 323
Db 295 EDPANTFTSTVQIPKVRSCPAEHLTCQP 324

RESULT 10
Q8CJ63 PRELIMINARY; PRT; 300 AA.
AC Q8CJ63;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Leukocyte cell-surface antigen isoform s.
GN Name=Slamf7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Thymus;
RX MEDLINE=22226696; PubMed=12242590; DOI=10.1007/s00251-002-0483-3;
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
RA Bosch J., Terhorst C., Engel P.;
RT "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of
RT leukocyte cell-surface receptors.";
RL Immunogenetics 54:394-402(2002).
DR EMBL; AF467911; AAN63160.1; -.
DR MGD; MGI:1922595; Slamf7.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 300 AA; 3332 MW; 9948108710EBEC3D CRC64;

Query Match 36.7%; Score 651; DB 2; Length 300;
Best Local Similarity 42.4%; Pred. No. 1.1e-45;

```

```

Matches 140; Conservative 50; Mismatches 92; Indels 48; Gaps 4;
QY 1 MAGSPTCLTLIIVLWLTGSAAGSPVKELVSGVGAFTPLKSKVKQVDSIVWTNTTPL 60
Db 1 MARFSTYIIFTSVLQCLITVTAASGTLKKVAGALDGSVFTLNLTEIKVDYVVTNTTFFL 60
QY 61 VTIOPEGGTIIIVTONRNRERVDPPGGYSLKSLKKNDSGIYVYGVYSSSLQOYSTOY 120
Db 61 AMVKKDG---VTSQSSNKERIVFPDGLYSMLKSLQKNDGSGAYRAEIVYSTSSQASLIQY 117
QY 121 VLHVYHLSPKPVTVMLGLOSNGKTCVNLTCMEHGEEDVIYTWKALGOAANESHGSL 180
Db 118 VLHVYKLSRPKVTIDRQSNKGTCTVNLTCSDQDGENVTYSKAVGQGNQFHDGATL 177
QY 181 PISRWGSDMTFICVARNPVSRNPFSSPILARKLCEGAADDPDSSMVLCLLLVPLLSL 240
Db 178 SIARSGEKDALTCWARPVNSFSTPVPQKLCEDAATDLTSLRGILYILCFSAVLIL 237
QY 241 FVLGLF---LWFLKRQEEYIEKKRVDICRETPNICPHSGENTYDTPHTNRTILK 296
Db 238 FAVLLTIPTHTTWIKKGRKP---EKKRVDHREQMPDLCFHLNEADYDTPYTKRRPE 259
QY 297 EDPANTVSTVTEIPKKMEN---PHSLLTMP 323
Db 260 EDPANTFTSTVQIPKVRSCPAEHLTCQP 289

RESULT 11
Q91XA0 PRELIMINARY; PRT; 294 AA.
AC Q91XA0;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Slamf7 protein.
GN Name=Slamf7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011154; AAH11154.1; -.
DR MGD; MGI:1922595; Slamf7.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR PROSITE; PS50835; IG_LIKE; 1.

```

RESULT 13  
09Z178

```

ID Q92178      PRELIMINARY;      PRT;      329 AA.
AC Q92178;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD84 leukocyte antigen.
GN Name=CD84; Synonyms=CD84;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peritoneum;
RX MEDLINE=99180614; PubMed=10079287; DOI=10.1007/s002510050490;
RA de la Fuente M.A., Tovar V., Pizcueta P., Nadal M., Bosch J.,
RA Engel P.;
RT "Molecular cloning, characterization, and chromosomal localization of
RT the mouse homologue of CD84, a member of the CD2 family of cell
RT surface molecules."
RL Immunogenetics 49:249-255(1999).
DR EMBL; AF043445; AD02273.1; -.
DR MGD; MGI:1336885; Cd84.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR SEQUENCE 329 AA; 37345 MW; 43BB1AA5AF1989E0 CRC64;

Query Match      20.5%; Score 362.5; DB 2; Length 329;
Best Local Similarity 30.5%; Pred. No. 1.1e-21;
Matches 105; Conservative 62; Mismatches 136; Indels 41; Gaps 14;

QY 11 IYVLTGSAAGPVKELV---GSVGGAVTPPLK-SKVQVDSIVMTNTPLVTIQP- 65
DB 8 IYVLTGSAAGPVKELV---GSVGGAVTPPLK-SKVQVDSIVMTNTPLVTIQP- 65
QY 66 -EGGTIIIVTQNNRRERVDPPDGGYSLKLSKLKNDSGIYVYSSSQPQSTQRYV 124
DB 67 VNKAETITQGYTKGRIEIDQYDVLRLMEDAGYKADINEEN-EEITIKYIYLI 125
QY 125 YEHLSKPKVTMGLOKNGKTCVTNLTCCMEHGEEDVIYTWKALGOAANESHGSLP 184
DB 126 YRLKTPKTIQSLISSLNTNITLTCSVEKEEDVTYSWSPFGKSN-----VLQ 179
QY 185 RWGESDMTFICVARNPVSNNFSSPILARKLCEGA-----ADDDSSMVLCLL 237
DB 180 SPMDQKLYTCTAQNPNVSNSSDSVTVQQPCTDTPSFHRAVLPGLAVLP 238
QY 238 LSLFVLGLFLWFLKRRQBEYIEEKRRVDICRETP-NICPHSGENTE---YD 293
DB 239 AFLRL-----YKRRDRIVLEAD---DVSKTYVAVVSRNAQPTESRIYDE 289
QY 294 ILKEDPANTVYTVETIPKKNENPHSLLTMPD--TPRLPAYENVI 335
DB 290 SCKDQPVTTIYSSVQLSEKMKETN---MKDRSLPKALGNETIV 329

RESULT 14
Q8W18      PRELIMINARY;      PRT;      339 AA.
AC Q8W18;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Leukocyte differentiation antigen CD84 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gaya A.;
```

```

RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y12632; CAA73181.1; -.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Signal.
FT SIGNAL.
FT CHAIN
FT SEQUENCE 339 AA; 38082 MW; E78D6D5CAC8D3604 CRC64;

Query Match      20.3%; Score 359; DB 2; Length 339;
Best Local Similarity 31.6%; Pred. No. 2.2e-21;
Matches 111; Conservative 51; Mismatches 143; Indels 46; Gaps 12;

QY 14 LWQL-----TGSAAAGPVKELV---GSVGGAVTPPLK-SKVQVDSIVMTNTPLVTIQ 64
DB 6 LWLILLCLQTWPEAAGKDSIEFTVNGILGESVTFPVNQKQVLIATSKTSVAYVTP 65
QY 65 PEGGT---IIVTQNNRRERVDPPDGGYSLKLSKLKNDSGIYVYSSSQPQSTQRYV 121
DB 66 GDSPTAPVTVTHRYNRYERIHAGPNVNLVSDLRMEDAGYKADINTQADPTTKRYN 125
QY 122 LHVYEHLSKPKVTMGLOKNGKTCVTNLTCCMEHGEEDVIYTWKALGOAANESHGSLP 181
DB 126 LQIVRRLGPKTIQSLSSLNTNITLTCSVEKEEDVTYSWSPFGKSN-----E 179
QY 182 ISRWGESDMTFICVARNPVSNNFSSPILARKLCEGAADDDPSSM-----VL 234
DB 180 IQPPEDEQLYCTAQNPNVSNSSDSISARQLC-----ADIAMGFRHTHTGLSL 232
QY 235 PLLLSLFLVLGLFLWFLKRRQ-----BEYIEEKRRV-DICRETNICPHSGENTE 284
DB 233 PFLVLILLSSVFLKRRQSCINTFTKPNYAAASKTIYTYIMASENTOP--AESRI 290
QY 285 DTIPIHTNRTILKEDPANTVYTVETIPKKNENPHSLLTMPDTPRLPAYENVI 335
DB 291 DEILQSKVLPKSEBPVNTVYSEVOFADKMGKASTQDSKP--PGTSSYEIVI 339

RESULT 15
Q6NZB6      PRELIMINARY;      PRT;      645 AA.
AC Q6NZB6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ly9 protein (Fragment).
GN Name=Ly9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heltan E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
```



**This Page Blank (uspto)**